

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 5, 2004, 14:09:33 ; Search time 54 Seconds  
(without alignments)  
544.166 Million cell updates/sec

Title: US-09-997-428-408  
Perfect score: 502  
Sequence: 1 MKIALLLGLCVALLSCSSAAA.....QAVGNVXKALLGALTVFG 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : A\_Geneseq\_29Jan04: \*  
1: Geneseq1980s: \*  
2: Geneseq1990s: \*  
3: Geneseq2000s: \*  
4: Geneseq2001s: \*  
5: Geneseq2002s: \*  
6: Geneseq2003as: \*  
7: Geneseq2003bs: \*  
8: Geneseq2004s: \*

pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	502	100.0	104	3	AAY66757 Membrane-
2	502	100.0	104	3	AAY44458 Human lun
3	502	100.0	104	3	AAY87288 Human sig
4	502	100.0	104	4	AAB65280 Human PRO
5	502	100.0	104	5	AAB6141 Human PRO
6	502	100.0	104	6	ABU58095 Human PRO
7	502	100.0	104	6	ABU59173 Novel hum
8	502	100.0	104	6	ABU82685 Human sec
9	502	100.0	104	6	ABU19895 Human sec
10	502	100.0	104	6	ABU60604 Human sec
11	502	100.0	104	6	ABU13986 Human PRO
12	502	100.0	104	6	ABU72571 Novel hum
13	502	100.0	104	6	ABU59320 Human sec
14	502	100.0	104	6	ABU26017 Human PRO
15	502	100.0	104	6	ABU59026 Human sec
16	502	100.0	104	6	ABU52404 Novel hum
17	502	100.0	104	6	ABU59469 Novel hum
18	502	100.0	104	6	ABU592235 Novel hum
19	502	100.0	104	6	ABU10941 Human PRO
20	502	100.0	104	6	ABU81693 Novel hum
21	502	100.0	104	6	ABU88632 Human sec
22	502	100.0	104	6	ABO34146 Human PRO
23	502	100.0	104	6	ADA37519 Human sec
24	502	100.0	104	6	ADA21605 Human sec
25	502	100.0	104	6	ADA10392 Human sec

99 160 31.9 93 6 ABO06270 Novel hum  
100 160 31.9 93 6 ABR59306 Abr59306 Human sec

ALIGNMENTS

RESULT 1  
AAV66757  
ID AAV66757 standard; protein; 104 AA.

XX AC AAY66757;  
XX DT 05-APR-2000 (first entry)  
XX DE Membrane-bound protein PRO1245.  
XX KW Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
XX KW pharmaceutical; receptor immunoadhesin; gene mapping.  
XX OS Homo sapiens.  
XX PN WO9963088-A2.  
XX PD 09-DEC-1999.  
XX PF 02-JUN-1999; 99WO-US012252.  
XX PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088722P.  
PR 10-JUN-1998; 98US-0088730P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088740P.  
PR 10-JUN-1998; 98US-0088741P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088811P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088825P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088863P.  
PR 12-JUN-1998; 98US-0089090P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.

18-JUN-1998; 98US-0089908P.  
19-JUN-1998; 98US-0089947P.  
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19-JUN-1998; 98US-0089952P.  
22-JUN-1998; 98US-0090246P.  
22-JUN-1998; 98US-0090252P.  
22-JUN-1998; 98US-0090254P.  
23-JUN-1998; 98US-0090349P.  
23-JUN-1998; 98US-0090355P.  
24-JUN-1998; 98US-0090429P.  
24-JUN-1998; 98US-0090431P.  
24-JUN-1998; 98US-0090435P.  
24-JUN-1998; 98US-0090444P.  
24-JUN-1998; 98US-0090445P.  
24-JUN-1998; 98US-0090461P.  
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24-JUN-1998; 98US-0090540P.  
24-JUN-1998; 98US-0090557P.  
25-JUN-1998; 98US-0090676P.  
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25-JUN-1998; 98US-0090690P.  
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26-JUN-1998; 98US-0090862P.  
26-JUN-1998; 98US-0090863P.  
01-JUL-1998; 98US-0091358P.  
02-JUL-1998; 98US-0091360P.  
02-JUL-1998; 98US-0091478P.  
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02-JUL-1998; 98US-0091519P.  
02-JUL-1998; 98US-0091544P.  
02-JUL-1998; 98US-0091628P.  
02-JUL-1998; 98US-0091628P.  
02-JUL-1998; 98US-0091633P.  
02-JUL-1998; 98US-0091646P.  
02-JUL-1998; 98US-0091673P.  
07-JUL-1998; 98US-0091978P.  
07-JUL-1998; 98US-0091982P.  
07-JUL-1998; 98US-0092182P.  
10-JUL-1998; 98US-0092472P.  
10-JUL-1998; 98US-0093339P.  
30-JUL-1998; 98US-0094651P.  
04-AUG-1998; 98US-0095282P.  
04-AUG-1998; 98US-0095285P.  
04-AUG-1998; 98US-0095301P.  
04-AUG-1998; 98US-0095302P.  
04-AUG-1998; 98US-0095318P.  
04-AUG-1998; 98US-0095321P.  
04-AUG-1998; 98US-0095325P.  
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10-AUG-1998; 98US-0095929P.  
10-AUG-1998; 98US-0096012P.  
10-AUG-1998; 98US-0096143P.  
11-AUG-1998; 98US-0096146P.  
12-AUG-1998; 98US-0096329P.  
17-AUG-1998; 98US-0096757P.  
17-AUG-1998; 98US-0096766P.  
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17-AUG-1998; 98US-0096791P.  
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17-AUG-1998; 98US-0096894P.  
17-AUG-1998; 98US-0096895P.  
17-AUG-1998; 98US-0096897P.  
18-AUG-1998; 98US-0096949P.  
18-AUG-1998; 98US-0096950P.  
18-AUG-1998; 98US-0096959P.

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PR 18-AUG-1998; 98US-0096960P.
PR 18-AUG-1998; 98US-0097022P.
PR 19-AUG-1998; 98US-0097141P.
PR 20-AUG-1998; 98US-0097218P.
PR 24-AUG-1998; 98US-0097661P.
PR 26-AUG-1998; 98US-0097951P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097952P.
PR 26-AUG-1998; 98US-0097955P.
PR 26-AUG-1998; 98US-0097971P.
PR 26-AUG-1998; 98US-0097974P.
PR 26-AUG-1998; 98US-0097978P.
PR 26-AUG-1998; 98US-0097979P.
PR 26-AUG-1998; 98US-0097986P.
PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
PR 16-SEP-1998; 98US-0100634P.
PR 12-JAN-1999; 99US-0115565P.
XX
PA (GETH ) GENENTECH INC.
XX
XX Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;
PI Wood WI, Yuan J;
XX
XX WPI; 2000-072883/06.
DR N-PSDB; AAZ65103.
XX
XX Membrane-bound proteins and related nucleotide sequences.
PT
XX
XX Claim 12; Fig 290; 822pp; English.
XX
XX The invention provides membrane-bound PRO polypeptides and
CC polynucleotides encoding them. The PRO sequences of the invention were
CC identified based on extracellular domain homology screening. The PRO
CC sequences have homology with proteins including LDL receptors, TIE
CC ligands and various enzymes. The membrane-bound proteins and receptor
CC molecules are useful as pharmaceutical and diagnostic agents. Receptor
CC immunoadhesins, for instance, can be used as therapeutic agents to block
CC receptor-ligand interactions. The membrane-bound proteins can also be
CC employed for screening of potential peptide or small molecule inhibitors
CC of the relevant receptor/ligand interaction. The PRO encoding sequences
CC are useful as hybridization probes, in chromosome and gene mapping and in
CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will
CC also be useful for the preparation of PRO polypeptides, especially by
CC recombinant techniques
XX
XX Sequence 104 AA;
SQ
Query Match 100.0%; Score 502; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLALLGLCVALLSCSSAAFLVGSAPVAPVVALESAAEAGAGTLANPLGTLNPKLL 60
DB 1 MKLALLGLCVALLSCSSAAFLVGSAPVAPVVALESAAEAGAGTLANPLGTLNPKLL 60
QY 61 LSSLGIPVNHIEGSKQVAGLGPQAVGAVKALKALGALTTFVG 104
DB 61 LSSLGIPVNHIEGSKQVAGLGPQAVGAVKALKALGALTTFVG 104
RESULT 2
AA44458
ID AAY44458 standard; protein; 104 AA.
XX
XX AAY44458;
XX
XX 27-MAR-2000 (first entry)
XX
XX Human lung specific gene protein lng107.
DE
XX
XX Lung Specific Gene; LSG; lng107; human; diagnostic marker; prognosticate;
KW lung cancer; diagnosis.
XX

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XX Homo sapiens.
XX OS
XX WO9960160-A1.
XX
XX 25-NOV-1999.
XX
XX 12-MAY-1999; 99WO-US010344.
XX
XX 21-MAY-1998; 98US-0086212P.
XX
XX (DIAD-) DIADEXUS LLC.
XX
XX Yang F, Macina RA, Sun Y;
XX WPI; 2000-116320/10.
XX N-PSDB; AAZ29723.
XX
XX A new method for diagnosing, monitoring and staging lung cancer.
PT
XX
XX Example 2; Page 38-39; 40pp; English.
XX
XX The present sequence is a lung specific gene (LSG) protein lng107 from
CC human clone ID 586271. The LSG has high level of tissue specificity for
CC lungs and is overexpressed in cancerous tissues. The sequence serves as a
CC diagnostic marker for detecting, monitoring, staging and prognosticating
CC lung cancer. The diagnosis involves comparing levels of LSG in samples
CC obtained from patient and normal control
XX
XX Sequence 104 AA;
SQ
Query Match 100.0%; Score 502; DB 3; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLALLGLCVALLSCSSAAFLVGSAPVAPVVALESAAEAGAGTLANPLGTLNPKLL 60
DB 1 MKLALLGLCVALLSCSSAAFLVGSAPVAPVVALESAAEAGAGTLANPLGTLNPKLL 60
QY 61 LSSLGIPVNHIEGSKQVAGLGPQAVGAVKALKALGALTTFVG 104
DB 61 LSSLGIPVNHIEGSKQVAGLGPQAVGAVKALKALGALTTFVG 104
RESULT 3
AA487288
ID AAY87288 standard; protein; 104 AA.
XX
XX AAY87288;
XX
XX 11-MAY-2000 (first entry)
XX
XX Human signal peptide containing protein HSPP-65 SEQ ID NO:65.
XX
XX Human; signal peptide-containing protein; HSPP; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; nootropic; neuroprotective; cardiovascular; hepatotropic;
KW antiasthmatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's diseases; ovulatory defect;
KW muscular dystrophy.
XX
XX Homo sapiens.
XX OS
XX WO200000610-A2.
XX
XX 06-JAN-2000.
XX
XX 25-JUN-1999; 99WO-US014484.
XX
XX 26-JUN-1998; 98US-0090762P.
XX

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PR 31-JUL-1998; 98US-0094983P.  
PR 01-OCT-1998; 98US-0102688P.  
PR 11-DEC-1998; 98US-0112129P.  
XX  
XX (INCYTE PHARM INC.  
XX PA  
XX PI Lal P, Tang VT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
PI Akerblom IE, Au-Young J, Yue H, Patterson C, Reddy R, Hillman JL;  
PI Bandman O;  
XX  
XX WPI; 2000-160673/14.  
DR N-PSDB; AA298173.  
DR  
XX PT New human signal peptide-containing proteins useful in treatment,  
PT prevention and diagnosis of e.g. cancer, inflammation and cardiovascular  
PT disease.  
XX  
XX Claim 1; Page 206; 327pp; English.  
PS  
XX AA298109 to AA298242 encode AA2987224 to AA2987357 which represent the  
CC human signal peptide-containing proteins HSP-1 to HSP-134. HSPs have  
CC anticancer, anti-inflammatory, antimicrobial, neurotropic, hepatotropic,  
CC neuroprotective, cardiovascular and antitumour activities, and can be  
CC used in gene therapy. HSPs can be used to treat or prevent disorders  
CC associated with decreased activity or function of HSP. Antagonists of  
CC HSP are used to treat or prevent disorders associated with increased  
CC activity or function of HSP. Such diseases include cell proliferation  
CC (including cancer), inflammation, cardiovascular, neurological,  
CC reproductive or developmental disorders, (e.g. arteriosclerosis,  
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
CC asthma, Crohn's disease, microbial or other infections, congestive or  
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's  
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP  
CC nucleic acids can be used for the recombinant production of HSP, for  
CC detecting HSP in standard hybridisation and amplification assays (for  
CC diagnosis and monitoring), in gene therapy, as antisense, triplex-forming  
CC or ribozyme therapeutics, for detecting related sequences or genetic  
CC variations, and for chromosomal mapping. HSP are also used to raise  
CC specific antibodies (Ab) and to screen for agonists and antagonists  
CC (potential therapeutic agents). Ab are used to diagnose, or monitor, HSP  
CC -related diseases (in usual immunoassays), as therapeutic antagonists, in  
CC competitive drug screens, and for purification of HSP from natural  
CC sources  
XX  
XX Sequence 104 AA;  
SQ  
Query Match 100.0%; Score 502; DB 3; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKLAALLGLCVALLSCSSAAAFVGSAPVQAQVVALESAAEAGAGTLANPLGTLNPLKLL 60  
Db 1 MKLAALLGLCVALLSCSSAAAFVGSAPVQAQVVALESAAEAGAGTLANPLGTLNPLKLL 60  
Qy 61 LSSLGIPVNHLEIGSQKVAELGPQAVGAVKALLGALTTFVG 104  
Db 61 LSSLGIPVNHLEIGSQKVAELGPQAVGAVKALLGALTTFVG 104  
RESULT 4  
AAB65280  
ID AAB65280 standard; protein; 104 AA.  
XX  
XX AAB65280;  
AC  
XX 02-APR-2001 (first entry)  
DT  
XX Human PRO1245 (UNQ629) protein sequence SEQ ID NO:408.  
DE  
XX Human; secreted and transmembrane protein; PRO; cytostatic; cell death;  
XX cancer; chromosomal mapping; gene mapping; tissue typing;  
KW diagnostic assay.  
KW  
XX

OS Homo sapiens.  
XX WO2000073454-A1.  
PN  
XX  
XX 07-DEC-2000.  
PD  
XX  
XX 30-MAR-2000; 2000WO-US008439.  
PF  
XX  
XX 02-JUN-1999; 99WO-US012352.  
PR 23-JUN-1999; 99US-0141037P.  
PR 23-JUL-1999; 99US-0143048P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 28-JUL-1999; 99US-0145688P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 08-OCT-1999; 99US-0158663P.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
XX  
XX (GETH ) GENENTECH INC.  
XX  
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
XX Grimaldi CJ, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;  
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
XX Zhang Z;  
XX WPI; 2001-032160/04.  
XX N-PSDB; AAF44249.  
XX  
XX PRO polynucleotides used to produce polypeptides used to target bioactive  
XX molecules such as toxins, radiolabels or antibodies, to specific cells,  
XX to cause targeted cell death.  
XX  
XX Claim 12; Fig 290; 935pp; English.  
XX  
XX The present invention describes human secreted and transmembrane PRO  
XX proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
XX be used for targeted delivery of bioactive molecules, such as toxins,  
XX radiolabels or antibodies, that cause cell death. PRO nucleotide  
XX sequences, and their fragments, can be used as hybridisation probes, in  
XX chromosomal and gene mapping, and in the generation of anti-sense RNA and  
XX DNA. They may also be used to produce transgenic animals which are used  
XX to develop and screen therapeutically useful reagents. The PRO nucleotide  
XX and protein sequence can be used for tissue typing and in treating  
XX cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to  
XX AAF44470 represent PCR primers and hybridisation probes used in the  
XX isolation of human PRO sequences. AAF44087 to AAF44269 and AAB65154 to  
XX AAB65300 represent human PRO polynucleotide and protein sequences given  
XX in the exemplification of the present invention  
XX  
XX Sequence 104 AA;  
SQ  
Query Match 100.0%; Score 502; DB 4; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
Qy 1 MKLAALLGLCVALLSCSSAAAFVGSAPVQAQVVALESAAEAGAGTLANPLGTLNPLKLL 60  
XX

Db 1 MKLALLGLCVALSCTSSAAFLVGSAPVQVVAALSAEAGAGTLANPLGTLNPLKLL 60  
QY 61 LSSLGIPVNHLEIGSQKCVAEELGPQAVGAVKALKALLGALTVEFG 104  
ID AAU86141 standard; protein; 104 AA.  
XX AAU86141;  
AC AAU86141;  
XX 15-JUL-2002 (first entry)  
DT Human PRO1245 polypeptide.  
XX Human; PRO; benign tumour; malignant tumour; lymphoid malignancy;  
KW leukaemia; neuronal disorder; stromal disorder; blastocoealic disorder;  
KW inflammatory disorder; immune disorder; angiogenic disorder; cytostatic;  
KW neuroprotective.  
XX Homo sapiens.  
OS WO200153486-A1.  
XX 26-JUL-2001.  
PD 11-FEB-2000; 2000WO-US003565.  
PF 08-MAR-1999; 99WO-US005028.  
XX 11-MAY-1999; 99US-0123972P.  
PR 11-MAY-1999; 99US-0133459P.  
PR 02-JUN-1999; 99WO-US012252.  
PR 22-JUN-1999; 99US-0140650P.  
PR 22-JUN-1999; 99US-0140653P.  
PR 20-JUL-1999; 99US-0144758P.  
PR 26-JUL-1999; 99US-0145698P.  
PR 28-JUL-1999; 99US-0146222P.  
PR 17-AUG-1999; 99US-0149395P.  
PR 31-AUG-1999; 99US-0151689P.  
PR 01-SEP-1999; 99WO-US020111.  
PR 15-SEP-1999; 99WO-US021090.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 01-DEC-1999; 99WO-US028634.  
PR 05-JAN-2000; 2000WO-US000219.  
XX (GETH ) GENENTECH INC.  
XX Ashkenazi AJ, Goddard A, Godowski PJ, Gurney AL, Hillan KJ;  
PI Marsters SA, Pan J, Pitti RM, Roy MA, Smith V, Stone DM;  
PI Watanabe CK, Wood WI;  
XX WPI; 2002-205567/26.  
DR N-PSDE; ABK40267.  
XX Thirty five nucleic acids encoding PRO polypeptides, useful for treating  
PT benign or malignant tumors, leukemias and lymphoid malignancies,  
FT inflammatory, angiogenic and immunologic disorders.  
XX Claim 61; Fig 28; 302pp; English.  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides and the polynucleotide sequences encoding them. The PRO  
CC polypeptides, agonists, antagonists or anti-PRO antibodies are useful for  
CC treating benign or malignant tumours (e.g. renal, kidney, bladder,  
CC breast, etc), leukemias and lymphoid malignancies, other disorders such  
CC as neuronal, glial, astrocytal, hypothalamic, glandular, macrophagal,  
CC stromal and blastocoealic disorders, inflammatory, immune and angiogenic  
CC disorders. The polynucleotide sequences are also useful in gene therapy.  
XX AAU86128-AAU86162 represent the human PRO polypeptides of the invention

SQ Sequence 104 AA;  
Query Match 100.0%; Score 502; DB 5; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLALLGLCVALSCTSSAAFLVGSAPVQVVAALSAEAGAGTLANPLGTLNPLKLL 60  
Db 1 MKLALLGLCVALSCTSSAAFLVGSAPVQVVAALSAEAGAGTLANPLGTLNPLKLL 60  
QY 61 LSSLGIPVNHLEIGSQKCVAEELGPQAVGAVKALKALLGALTVEFG 104  
Db 61 LSSLGIPVNHLEIGSQKCVAEELGPQAVGAVKALKALLGALTVEFG 104  
RESULT 6  
ABUS8095  
ID ABUS8095 standard; protein; 104 AA.  
XX ABUS8095;  
AC ABUS8095;  
XX 14-APR-2003 (first entry)  
DT Human PRO polypeptide #127.  
XX Human; PRO; cytostatic; tumour; cancer; breast; lung; stomach; liver;  
KW horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT;  
KW antibody-dependent enzyme mediated prodrug therapy.  
XX Homo sapiens.  
OS US2003027163-A1.  
XX 06-FEB-2003.  
PD 15-NOV-2001; 2001US-00997666.  
PF 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
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PR	17-AUG-1998;	98US-0096773P.			
PR	17-AUG-1998;	98US-0096791P.			



PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes  
PT are therapeutically useful for enhancing immune response and in cancer  
treatments.

XX Claim 12; Fig 290; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO  
CC polypeptides are useful in detecting PRO polypeptides in a sample, in  
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and  
CC in modulating at least one biological activity of a cell expressing a PRO  
CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus  
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186  
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,  
CC PRO943, PRO828, PRO826, PRO819, PRO1126,  
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus  
CC useful for treating conditions or disorders where angiogenesis would be  
CC beneficial, e.g. wound healing and antagonist of this polypeptide are  
CC useful for treating cancerous tumours. PRO812 inhibits vascular  
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial  
CC cells and is thus useful for inhibiting endothelial cell growth in  
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,  
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of  
CC stimulated T-lymphocytes and are therapeutically useful for enhancing  
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of  
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of  
CC rod photoreceptor cells) and therefore are useful for treating retinal  
CC disorders of injuries, e.g. retinitis pigmentosa, AMD. PRO819, PRO813  
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,  
CC and therefore are useful for treating kidney disorders associated with  
CC decreased mesangial cell function such as Berger disease or other  
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's  
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the  
CC proliferation and/or redifferentiation of chondrocytes in culture and are  
CC thus useful for treating sports injuries and arthritis. This is the  
CC amino acid sequence of a novel human PRO protein

XX Sequence 104 AA;

Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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DB 1 MKLAALLGLCVALLSCSSAAFLVGSAAKPAQVAALESAAEAGCTLANPLGTINPLKLL 60  
QY 61 LSSLGIPVNHLEGSQKCVAEIQPQAVGAVKALKALLGALTIVFG 104  
DB 61 LSSLGIPVNHLEGSQKCVAEIQPQAVGAVKALKALLGALTIVFG 104

RESULT 8

ABU82685  
ID ABU82685 standard; protein; 104 AA.

XX AC ABU82685;

XX 26-JUN-2003 (first entry)

DE Human secreted/transmembrane protein PRO1245.

XX Human; PRO; secreted protein; transmembrane protein;  
KW cardiac insufficiency disorders; angiogenesis; wound healing;  
KW cancerous tumour; immune response; retinal disorder; sight loss;  
KW retinitis pigmentosa; age-related macular degeneration; AMD;  
KW kidney disorder; Berger disease; nephropathy; dermatitis; herpeticiformis;  
KW Crohn's disease; sports injury; arthritis.

XX Homo sapiens.

XX US2003032023-A1.

XX

PD 13-FEB-2003.  
XX 14-NOV-2001; 2001US-00990711.  
XX 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US020069.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0085311P.  
PR 24-NOV-1997; 97US-0086770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
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PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
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PR 01-OCT-1998; 98WO-US021141.  
PR 07-DEC-1998; 98WO-US025108.  
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PR 08-MAR-1999; 98WO-US005028.  
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PR 16-DEC-1999; 99WO-US028634.  
PR 20-DEC-1999; 99WO-US030095.  
PR 05-JAN-2000; 99WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
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PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
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PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.

Query Match 100.0%; Score 502; DB 6; Length 104;

Best Local Similarity 100.0%; Pred.No.1.4e-48; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKLAALIGLCVALSCSSAAAFVLGSAKPVAQFVAALSAEAGAGTLANPLGTLPKLL 60

Qy 61 LSSIGIPVNHIEGSKVVAELGPQAVGAVKALKALIGALTVEG 104

Db 61 LSSIGIPVNHIEGSKVVAELGPQAVGAVKALKALIGALTVEG 104

#### RESULT 9

AAO19895  
ID AAO19895 standard; protein; 104 AA.  
XX AC AAO19895;  
XX DT 11-AUG-2003 (first entry)  
XX DE Human uteroglobin related protein 2.  
XX KW UGRP1; human; mouse; promoter; uteroglobin related protein 1;  
XX KW respiratory disorder; asthma.  
XX OS Homo sapiens.  
XX PN WO2003000111-A2.  
XX PD 03-JAN-2003.  
XX PF 18-JUN-2002; 2002WO-US019456.  
XX PR 20-JUN-2001; 2001US-0299828P.  
XX PA (USSH ) US DEPT HEALTH & HUMAN SERVICES.

XX Kimura S, Niimi T;  
PI WPI; 2003-184004/18.  
XX  
XX New human UGRPI nucleic acid, useful for diagnosing or predicting a  
PT predisposition to develop a respiratory disorder or determining the  
PT prognosis of a subject having or suspected of having a respiratory  
PT disorder e.g., asthma.  
XX  
XX Disclosure; Page 79-80; 83pp; English.  
XX  
XX The present invention provides the human and murine uteroglobin related  
CC protein 1 (UGRP1) promoters. The sequences can be used in the diagnosis  
CC of and prediction of predisposition to respiratory disorders such as  
CC asthma. The present sequence is a protein sequence shown in the  
CC exemplification of the invention  
XX  
XX Sequence 104 AA;  
SQ  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
QY 1 MKLAALLGLCVLSCSSAAFLVGSAPVAQVAALESAAEAGATLANPLGTLNPLKLL 60  
DB 1 MKLAALLGLCVLSCSSAAFLVGSAPVAQVAALESAAEAGATLANPLGTLNPLKLL 60  
QY 61 LSSLGIPVNHLEGSQKVAELGPQAVGAVKALLGALTVEG 104  
DB 61 LSSLGIPVNHLEGSQKVAELGPQAVGAVKALLGALTVEG 104  
RESULT 10  
ABUS0604  
ID ABUS0604 standard; protein; 104 AA.  
XX  
XX AC ABUS0604;  
XX  
XX DT 01-MAY-2003 (first entry)  
XX  
XX DE Human secreted/transmembrane protein, #163.  
XX  
XX KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;  
KW diagnostic; therapeutic; gene therapy.  
XX  
XX OS Homo sapiens.  
XX  
XX PN US2002160384-A1.  
XX  
XX PD 31-OCT-2002.  
XX  
XX PF 14-NOV-2001; 2001US-00992598.  
XX  
XX PR 16-JUN-1997; 97US-0049787P.  
XX PR 17-OCT-1997; 97US-0062250P.  
XX PR 05-NOV-1997; 97WO-US020069.  
XX PR 12-NOV-1997; 97US-0065186P.  
XX PR 13-NOV-1997; 97US-0065311P.  
XX PR 24-NOV-1997; 97US-0066770P.  
XX PR 25-FEB-1998; 98US-0075945P.  
XX PR 20-MAR-1998; 98US-0078910P.  
XX PR 28-APR-1998; 98US-0083322P.  
XX PR 07-MAY-1998; 98US-0084600P.  
XX PR 28-MAY-1998; 98US-0087106P.  
XX PR 02-JUN-1998; 98US-0087609P.  
XX PR 02-JUN-1998; 98US-0087759P.  
XX PR 03-JUN-1998; 98US-0087827P.  
XX PR 04-JUN-1998; 98US-0088021P.  
XX PR 04-JUN-1998; 98US-0088025P.  
XX PR 04-JUN-1998; 98US-0088026P.  
XX PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.  
PR 18-JUN-1998; 98US-0089908P.  
PR 15-SEP-1998; 98WO-US019330.  
PR 17-SEP-1998; 98WO-US019437.  
PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US023108.  
PR 05-JAN-1999; 99WO-US000106.  
PR 08-MAR-1999; 99WO-US005028.  
PR 02-JUN-1999; 99WO-US012252.  
PR 15-SEP-1999; 99WO-US021090.  
PR 15-SEP-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US028634.  
PR 16-DEC-1999; 99WO-US030095.  
PR 20-DEC-1999; 99WO-US030911.  
PR 06-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 24-FEB-2000; 2000WO-US005004.  
PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUN-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023328.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.

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PR 28-AUG-2001; 2001US-00941992.
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL,
PI Perrara N, Fong S, Garber H, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Kljavin IV, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PI Zhang Z;
XX
XX WPI; 2003-288106/28.
DR N-PSDB; ABX90363.
XX
XX New transmembrane polypeptides and nucleic acids encoding the
PT polypeptides, useful in gene therapy, in chromosome identification, as
PT chromosome markers, or in generating probes.
XX
XX Claim 12; Fig 290; 650pp; English.
XX
XX The invention discloses isolated PRO secreted/transmembrane polypeptides
CC comprising a sequence without signal peptide and the nucleic acid
CC encoding them. The polypeptides can be used to raise antibodies that
CC specifically bind to the PRO polypeptide, for linking a bioactive
CC molecule to a cell expressing a PRO protein and for modulating at least
CC one biological activity of a cell. The PRO polypeptides or
CC polynucleotides are also useful in gene therapy, in chromosome
CC identification, as chromosome markers, or in generating probes. The PRO
CC polypeptides are useful as molecular markers for protein electrophoresis,
CC and the isolated nucleic acids may be used for recombinantly expressing
CC these markers. The PRO polypeptides and nucleic acids may also be used in
CC tissue typing. Anti-PRO antibodies are useful in diagnostic assays for
CC PRO, and in affinity purification of PRO from recombinant cell culture or
CC natural sources. The sequences presented in ABU60478-ABU60624 are the PRO
CC polynucleotides of the invention. Note: The sequence data for this patent
CC is also available in electronic format from USPTO at
CC seqdata.uspto.gov/sequence.html
XX
XX Sequence 104 AA;
SQ
Query Match 100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAALLGLCVALSCTSSAAAFVLSAKFVAQPVAALESAAEAGAGTLANPLGTLNPKLL 60
Db 1 MKLAALLGLCVALSCTSSAAAFVLSAKFVAQPVAALESAAEAGAGTLANPLGTLNPKLL 60
QY 61 LSSLGIPVNHLEIGSKCVAEELGPAVGAKVALLGALTIVFG 104
Db 61 LSSLGIPVNHLEIGSKCVAEELGPAVGAKVALLGALTIVFG 104
RESULT 11
ABU13986
ID ABU13986 standard; protein; 104 AA.
XX
XX AC ABU13986;
XX
XX 26-FEB-2003 (first entry)
XX
XX Human PRO1245 polypeptide.
XX
XX Human; PRO polypeptide; secreted protein; transmembrane protein;
XX genetic disorder; antibacterial; immunosuppressive.
XX
XX Hmo sapiens.
XX
XX US2002103125-A1.
XX
XX 01-AUG-2002.
XX
XX 20-NOV-2001; 2001US-00989731.
XX
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16-JUN-1997; 97US-0049787P.  
17-OCT-1997; 97US-0062250P.  
05-NOV-1997; 97WO-US020069.  
12-NOV-1997; 97US-0065311P.  
13-NOV-1997; 97US-0066770P.  
24-NOV-1997; 98US-0075945P.  
25-FEB-1998; 98US-0078910P.  
28-APR-1998; 98US-0083322P.  
28-MAY-1998; 98US-0084600P.  
28-MAY-1998; 98US-0087106P.  
02-JUN-1998; 98US-0087607P.  
02-JUN-1998; 98US-0087609P.  
02-JUN-1998; 98US-0087759P.  
03-JUN-1998; 98US-0087827P.  
04-JUN-1998; 98US-0088021P.  
04-JUN-1998; 98US-0088025P.  
04-JUN-1998; 98US-0088026P.  
04-JUN-1998; 98US-0088028P.  
04-JUN-1998; 98US-0088029P.  
04-JUN-1998; 98US-0088030P.  
04-JUN-1998; 98US-0088033P.  
04-JUN-1998; 98US-0088326P.  
05-JUN-1998; 98US-0088367P.  
05-JUN-1998; 98US-0088820P.  
05-JUN-1998; 98US-0088821P.  
05-JUN-1998; 98US-0088821P.  
09-JUN-1998; 98US-0088655P.  
10-JUN-1998; 98US-0088734P.  
10-JUN-1998; 98US-0088738P.  
10-JUN-1998; 98US-0088742P.  
10-JUN-1998; 98US-0088810P.  
10-JUN-1998; 98US-0088824P.  
10-JUN-1998; 98US-0088826P.  
11-JUN-1998; 98US-0088858P.  
11-JUN-1998; 98US-0088861P.  
11-JUN-1998; 98US-0088876P.  
12-JUN-1998; 98US-0089105P.  
16-JUN-1998; 98US-0089440P.  
16-JUN-1998; 98US-0089512P.  
16-JUN-1998; 98US-0089514P.  
17-JUN-1998; 98US-0089532P.  
17-JUN-1998; 98US-0089538P.  
17-JUN-1998; 98US-0089598P.  
17-JUN-1998; 98US-0089599P.  
17-JUN-1998; 98US-0089600P.  
17-JUN-1998; 98US-0089653P.  
18-JUN-1998; 98US-0089801P.  
18-JUN-1998; 98US-0089907P.  
18-JUN-1998; 98US-0089908P.  
16-SEP-1998; 98WO-US019330.  
17-SEP-1998; 98WO-US019437.  
07-OCT-1998; 98WO-US021141.  
01-DEC-1998; 98WO-US025108.  
05-JAN-1999; 99WO-US000106.  
08-MAR-1999; 99WO-US005028.  
02-JUN-1999; 99WO-US012252.  
15-SEP-1999; 99WO-US021090.  
15-SEP-1999; 99WO-US021547.  
30-NOV-1999; 99WO-US028313.  
01-DEC-1999; 99WO-US028301.  
01-DEC-1999; 99WO-US028634.  
16-DEC-1999; 99WO-US030095.  
20-DEC-1999; 99WO-US030911.  
06-JAN-2000; 2000WO-US000219.  
06-JAN-2000; 2000WO-US000376.  
11-FEB-2000; 2000WO-US003565.  
18-FEB-2000; 2000WO-US004341.  
22-FEB-2000; 2000WO-US004414.  
24-FEB-2000; 2000WO-US004914.  
24-FEB-2000; 2000WO-US005004.  
02-MAR-2000; 2000WO-US005841.  
10-MAR-2000; 2000WO-US006319.

PR 15-MAR-2000; 2000WO-US006884.  
PR 20-MAR-2000; 2000WO-US007377.  
PR 30-MAR-2000; 2000WO-US008439.  
PR 15-MAY-2000; 2000WO-US013358.  
PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 30-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.  
PR 23-AUG-2000; 2000WO-US023522.  
PR 24-AUG-2000; 2000WO-US023528.  
PR 08-NOV-2000; 2000WO-US030952.  
PR 01-DEC-2000; 2000WO-US032678.  
PR 28-FEB-2001; 2001WO-US006520.  
PR 01-JUN-2001; 2001WO-US017800.  
PR 20-JUN-2001; 2001WO-US019692.  
PR 29-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.

(GETH ) GENENTECH LTD.

PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;  
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;  
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF;  
PI Roy MA, Stewart TA, Tunas D, Watanabe CK, Williams PM, Wood WJ;  
PI Zhang Z;

XX WPI; 2003-102117/09.  
DR N-PSDB; ABX64209.

XX Novel secreted and transmembrane polypeptide for modulating biological  
PT activity of cell expressing the polypeptide, identifying agonists or  
PT antagonists of polypeptide, and as molecular weight markers.

XX Claim 12; Fig 290; 64pp; English.

XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
CC biological activities of cells expressing PRO polypeptides, and for for  
CC identifying agonists or antagonists. The polynucleotide sequences  
CC encoding PRO polypeptides are useful as hybridisation probes in  
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,  
CC in the preparation of PRO polypeptides, for generating transgenic animals  
CC or knockout animals, to construct hybridisation probes for mapping the  
CC gene which encodes the PRO polypeptide, and for the genetic analysis of  
CC individuals with genetic disorders, in gene therapy, for chromosome  
CC identification, as chromosome markers, and for generating probes for PCR,  
CC Northern analysis, Southern analysis and Western analysis. ABU13860-  
CC ABU14006 represent the human PRO polypeptides of the invention. Note: The  
CC sequence data for this patent was obtained in electronic format directly  
CC from the USPTO web site at seqdata.uspto.gov/psipdbEntry.html

XX Sequence 104 AA;

Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. NO. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALGLCVLSCSSAAAFVLSGAKPVAQPVAALESAAAGAGTLANPLGLNPKLL 60  
Db 1 MKLAALGLCVLSCSSAAAFVLSGAKPVAQPVAALESAAAGAGTLANPLGLNPKLL 60  
QY 61 LSSLGIPVNHLEGSQKCVAELOPQAVGAVKALKALGALTTFG 104  
Db 61 LSSLGIPVNHLEGSQKCVAELOPQAVGAVKALKALGALTTFG 104

RESULT 12

ABU72571  
ID ABU72571 standard; protein; 104 AA.  
XX AC ABU72571;  
XX DT 17-JUN-2003 (first entry)  
XX DE Novel human secreted and transmembrane protein PRO1245.  
XX KW Human; secreted and transmembrane protein; cytostatic; anti-HIV;  
KW virucide; hepatotropic; antiinflammatory; neuroprotective; gene therapy;  
KW PRO; pharmaceutical; diagnostic; biosensor; bioindicator; malignancy;  
KW cancer; ovarian cancer; colorectal cancer; Kaposi's sarcoma; leukaemia;  
KW lymphoma; hepatitis B; multiple sclerosis; Crohn's disease;  
KW drug screening.  
XX OS Homo sapiens.  
XX PN US2003003531-A1.  
XX PD 02-JAN-2003.  
XX PF 19-NOV-2001; 2001US-00989734.  
XX PR 16-JUN-1997; 97US-0049787P.  
PR 17-OCT-1997; 97US-0062250P.  
PR 05-NOV-1997; 97WO-US02006P.  
PR 12-NOV-1997; 97US-0065186P.  
PR 13-NOV-1997; 97US-0065311P.  
PR 24-NOV-1997; 97US-0066770P.  
PR 25-FEB-1998; 98US-0075945P.  
PR 20-MAR-1998; 98US-0078910P.  
PR 28-APR-1998; 98US-0083322P.  
PR 07-MAY-1998; 98US-0084600P.  
PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
PR 02-JUN-1998; 98US-0087609P.  
PR 02-JUN-1998; 98US-0087759P.  
PR 03-JUN-1998; 98US-0087827P.  
PR 04-JUN-1998; 98US-0088021P.  
PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
PR 04-JUN-1998; 98US-0088030P.  
PR 04-JUN-1998; 98US-0088033P.  
PR 04-JUN-1998; 98US-0088326P.  
PR 05-JUN-1998; 98US-0088167P.  
PR 05-JUN-1998; 98US-0088202P.  
PR 05-JUN-1998; 98US-0088212P.  
PR 05-JUN-1998; 98US-0088217P.  
PR 09-JUN-1998; 98US-0088655P.  
PR 10-JUN-1998; 98US-0088734P.  
PR 10-JUN-1998; 98US-0088738P.  
PR 10-JUN-1998; 98US-0088742P.  
PR 10-JUN-1998; 98US-0088810P.  
PR 10-JUN-1998; 98US-0088824P.  
PR 10-JUN-1998; 98US-0088826P.  
PR 11-JUN-1998; 98US-0088858P.  
PR 11-JUN-1998; 98US-0088861P.  
PR 11-JUN-1998; 98US-0088876P.  
PR 12-JUN-1998; 98US-0089105P.  
PR 16-JUN-1998; 98US-0089440P.  
PR 16-JUN-1998; 98US-0089512P.  
PR 16-JUN-1998; 98US-0089514P.  
PR 17-JUN-1998; 98US-0089532P.  
PR 17-JUN-1998; 98US-0089538P.  
PR 17-JUN-1998; 98US-0089598P.  
PR 17-JUN-1998; 98US-0089599P.  
PR 17-JUN-1998; 98US-0089600P.  
PR 17-JUN-1998; 98US-0089653P.  
PR 18-JUN-1998; 98US-0089801P.  
PR 18-JUN-1998; 98US-0089907P.

PR 18-JUN-1998; 98US-0089908P.  
 PR 16-SEP-1998; 98WO-US019330.  
 PR 17-SEP-1998; 98WO-US019437.  
 PR 07-OCT-1998; 98WO-US021141.  
 PR 01-DEC-1998; 98WO-US025108.  
 PR 05-JAN-1999; 99WO-US000106.  
 PR 08-MAR-1999; 99WO-US005028.  
 PR 02-JUN-1999; 99WO-US012252.  
 PR 15-SEP-1999; 99WO-US021090.  
 PR 15-SEP-1999; 99WO-US021547.  
 PR 30-NOV-1999; 99WO-US028313.  
 PR 01-DEC-1999; 99WO-US028301.  
 PR 01-DEC-1999; 99WO-US028634.  
 PR 16-DEC-1999; 99WO-US030095.  
 PR 20-DEC-1999; 99WO-US030911.  
 PR 05-JAN-2000; 2000WO-US000219.  
 PR 06-JAN-2000; 2000WO-US000376.  
 PR 11-FEB-2000; 2000WO-US003565.  
 PR 18-FEB-2000; 2000WO-US004341.  
 PR 22-FEB-2000; 2000WO-US004414.  
 PR 24-FEB-2000; 2000WO-US004914.  
 PR 24-FEB-2000; 2000WO-US005004.  
 PR 02-MAR-2000; 2000WO-US005841.  
 PR 10-MAR-2000; 2000WO-US006319.  
 PR 15-MAR-2000; 2000WO-US006884.  
 PR 20-MAR-2000; 2000WO-US007377.  
 PR 30-MAR-2000; 2000WO-US008439.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 28-JUL-2000; 2000WO-US020710.  
 PR 11-AUG-2000; 2000WO-US022031.  
 PR 23-AUG-2000; 2000WO-US023522.  
 PR 08-NOV-2000; 2000WO-US023328.  
 PR 01-DEC-2000; 2000WO-US030952.  
 PR 28-FEB-2001; 2001WO-US006520.  
 PR 01-JUN-2001; 2001WO-US017800.  
 PR 20-JUN-2001; 2001WO-US019892.  
 PR 29-JUN-2001; 2001WO-US021066.  
 PR 09-JUL-2001; 2001WO-US021735.  
 PR 28-AUG-2001; 2001WO-US0941992.

(GETH ) GENENTECH INC.

PR Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,  
 PI Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,  
 PI Grimaldi JC, Gurney AL, Kiljavin LJ, Napier MA, Pan J, Paoni NF,  
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,  
 PI Zhang Z;

DR WPI; 2003-352829/33.  
 DR N-PSDB; ACA64431.

XX New genes and secreted and transmembrane polypeptides (e.g. PRO183 or  
 XX PRO184), useful for treating or diagnosing e.g. ovarian cancer, Kaposi's  
 PT sarcoma, leukemia, lymphoma, hepatitis B, multiple sclerosis or Crohn's  
 PT disease.

XX Claim 12; Fig 290; 663pp; English.

XX The invention describes a new isolated nucleic acid molecule comprising  
 CC the full length coding sequence of the DNA deposited with the American  
 CC Type Culture Collection (e.g. ATCC Deposit No. 209621, 552-PTA, 819-PTA,  
 CC 209439, 203135, etc.) or a sequence with at least 80% identity to a DNA  
 CC encoding a PRO polypeptide. The PRO polypeptides or polynucleotides are  
 CC useful as pharmaceuticals, diagnostics, biosensors or bioeffectors. These  
 CC are particularly useful for detecting or treating e.g. malignancies or  
 CC cancers (e.g. ovarian cancer, colorectal cancer, Kaposi's sarcoma,  
 CC leukemia or lymphoma), hepatitis B, multiple sclerosis, or Crohn's  
 CC disease in mammals. The PRO polypeptides are useful in drug screening,

CC particularly as targets for therapeutic intervention in these diseases,  
 CC and in the diagnostic determination of the presence of these diseases.  
 CC The PRO polypeptides are also useful as molecular weight markers, or for  
 CC chromosome identification. The PRO genes are useful as hybridisation  
 CC probes, or for screening libraries of human cDNA, genomic DNA or mRNA.  
 CC The PRO genes may also be used in gene therapy, particularly for a novel  
 CC replacing a defective gene. This is the amino acid sequence of a novel  
 CC human secreted and transmembrane PRO polypeptide  
 XX  
 SQ Sequence 104 AA;

Query Match 100.0%; Score 502; DB 6; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-48; Mismatches 0; Gaps 0;  
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Qy 1 MKLAALLGLCVALLSCSSAAAFVLSAKPVAQPVAALESAAEAGAGTLANPLKLL 60  
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# RESULT 13

ABU59320  
 ID ABU59320 standard; protein; 104 AA.

XX AC ABU59320;

XX DT 22-APR-2003 (first entry)

XX DE Human secreted/transmembrane protein, #163.

XX KW Human; PRO; secreted; transmembrane; pharmaceutical; diagnostic;  
 KW biosensor; bioeffector; tumour; therapeutic; gene therapy;  
 KW tumour-associated antigenic target; TAT; ADEPT;  
 KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.

XX OS Homo sapiens.

XX FN US2003027162-A1.

XX PD 06-FEB-2003.

XX PF 15-NOV-2001; 2001US-00997428.

XX PR 16-JUN-1997; 97US-0049787P.

XX PR 17-OCT-1997; 97US-0062250P.

XX PR 05-NOV-1997; 97WO-US020069.

XX PR 12-NOV-1997; 97US-0065186P.

XX PR 13-NOV-1997; 97US-0065311P.

XX PR 24-NOV-1997; 97US-0066770P.

XX PR 25-FEB-1998; 98US-0075945P.

XX PR 20-MAR-1998; 98US-0078310P.

XX PR 28-APR-1998; 98US-0083322P.

XX PR 07-MAY-1998; 98US-0084600P.

XX PR 28-MAY-1998; 98US-0087106P.

XX PR 02-JUN-1998; 98US-0087607P.

XX PR 02-JUN-1998; 98US-0087609P.

XX PR 03-JUN-1998; 98US-0087759P.

XX PR 04-JUN-1998; 98US-0087827P.

XX PR 04-JUN-1998; 98US-0088021P.

XX PR 04-JUN-1998; 98US-0088025P.

XX PR 04-JUN-1998; 98US-0088026P.

XX PR 04-JUN-1998; 98US-0088028P.

XX PR 04-JUN-1998; 98US-0088029P.

XX PR 04-JUN-1998; 98US-0088030P.

XX PR 04-JUN-1998; 98US-0088033P.

XX PR 04-JUN-1998; 98US-0088326P.

XX PR 05-JUN-1998; 98US-0088167P.

XX PR 05-JUN-1998; 98US-0088202P.

XX PR 05-JUN-1998; 98US-0088212P.

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PR	24-JUN-1998;	98US-0090429P.	PR	16-SEP-1998;	98US-0100634P.
PR	24-JUN-1998;	98US-0090431P.	PR	16-SEP-1998;	98MO-US019330.
PR	24-JUN-1998;	98US-0090433P.	PR	17-SEP-1998;	98US-0106858P.
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PR	24-JUN-1998;	98US-0090472P.	PR	07-OCT-1998;	98MO-US021141.
PR	24-JUN-1998;	98US-0090533P.	PR	01-DEC-1998;	98MO-US025108.
PR	24-JUN-1998;	98US-0090540P.	PR	22-DEC-1998;	98US-0113296P.
PR	24-JUN-1998;	98US-0090542P.	PR	05-JAN-1999;	98MO-US000106.
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PR	25-JUN-1998;	98US-0090695P.	PR	20-JUL-1999;	98US-0144758P.
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PR	01-JUL-1998;	98US-0091360P.	PR	15-SEP-1999;	98MO-US021090.
PR	01-JUL-1998;	98US-0091544P.	PR	15-SEP-1999;</	

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PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 26-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.

Query Match      100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 MKLAALIGLCVSLSCSARAFVGSAPVAPVALESAAEAGAGTLANPLGTLNPLKLL 60

Oy 61 LSSLGIPVNHLEIGSKVCVAELGPQAVGAVKALKALLGALTVPFG 104
Db 61 LSSLGIPVNHLEIGSKVCVAELGPQAVGAVKALKALLGALTVPFG 104

RESULT 14
ABO26017
ID ABO26017 standard; protein; 104 AA.
XX AC ABO26017;
XX DT 10-SEP-2003 (first entry)
XX DE Human PRO1245 polypeptide.
XX KW Human; PRO polypeptide; secreted protein; transmembrane protein;
XX OS genetic disorder; antibacterial; immunosuppressive.
XX OS Homo sapiens.
XX PN US2002127576-A1.
XX PD 12-SEP-2002.
XX PF 14-NOV-2001; 2001US-00991073.
XX PR 16-JUN-1997; 97US-0049787P.
XX PR 17-OCT-1997; 97US-0062250P.
XX PR 05-NOV-1997; 97WO-US020069.
XX PR 12-NOV-1997; 97US-0065186P.
XX PR 13-NOV-1997; 97US-0065311P.
XX PR 24-NOV-1997; 97US-0066770P.
XX PR 25-FEB-1998; 98US-0075945P.
XX PR 20-MAR-1998; 98US-0078940P.
XX PR 28-APR-1998; 98US-0083322P.
XX PR 07-MAY-1998; 98US-0084600P.
XX PR 28-MAY-1998; 98US-0087106P.
XX PR 02-JUN-1998; 98US-0087607P.
XX PR 02-JUN-1998; 98US-0087609P.
XX PR 02-JUN-1998; 98US-0087759P.
XX PR 03-JUN-1998; 98US-0087827P.
XX PR 04-JUN-1998; 98US-0088021P.
XX PR 04-JUN-1998; 98US-0088025P.
XX PR 04-JUN-1998; 98US-0088026P.
XX PR 04-JUN-1998; 98US-0088028P.
XX PR 04-JUN-1998; 98US-0088029P.
XX PR 04-JUN-1998; 98US-0088030P.
XX PR 04-JUN-1998; 98US-0088033P.
XX PR 04-JUN-1998; 98US-0088326P.
XX PR 05-JUN-1998; 98US-0088167P.
XX PR 05-JUN-1998; 98US-0088202P.
XX PR 05-JUN-1998; 98US-0088212P.
XX PR 05-JUN-1998; 98US-0088217P.
XX PR 09-JUN-1998; 98US-0088655P.
XX PR 10-JUN-1998; 98US-0088734P.
XX PR 10-JUN-1998; 98US-0088738P.
XX PR 10-JUN-1998; 98US-0088742P.

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PR 17-JUN-1998; 98US-0089653P.
PR 18-JUN-1998; 98US-0089801P.
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PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
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PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US021108.
PR 05-JAN-1999; 99WO-US000106.
PR 08-MAR-1999; 99WO-US005028.
PR 02-JUN-1999; 99WO-US012252.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 01-DEC-1999; 99WO-US028634.
PR 16-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 06-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US005004.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 08-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.

( GETH ) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Denoyers L, Eaton DL,
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Kijavini IJ, Napier MA, Pan J, Paoni NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
XX Zhang Z;
XX MPI, 2003-340824/32.
DR N-FSDB; ACD44399.
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XX Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346  
PT and PRO1375 which stimulate proliferation of stimulated T-lymphocytes  
PT and are therapeutically useful for enhancing immune responses.  
XX Claim 12; Fig 290; 66pp; English.  
XX The present invention relates to the isolation of novel human PRO  
CC polypeptides, and the polynucleotide sequences encoding them. The PRO  
CC polypeptides are secreted and transmembrane proteins. The PRO  
CC polypeptides are useful for detecting other PRO polypeptides, for linking  
CC bioactive molecules to cells expressing PRO polypeptides, for modulating  
CC biological activities of cells expressing PRO polypeptides, and for  
CC identifying agonists or antagonists. The polynucleotide sequences  
CC encoding PRO polypeptides are useful as hybridisation probes, in  
CC chromosome and gene mapping, in the generation of antisense RNA and DNA,  
CC in the preparation of PRO polypeptides, for generating transgenic animals  
CC or knockout animals, to construct hybridisation probes for mapping the  
CC gene which encodes the PRO polypeptide, and for the genetic analysis of  
CC individuals with genetic disorders, in gene therapy, for chromosome  
CC identification, as chromosome markers, and for generating probes for PCR,  
CC Northern analysis, Southern analysis and Western analysis. ABO2891-  
CC ABO26037 represent the human PRO polypeptides of the invention. Note: The  
CC sequence data for this patent was obtained in electronic format directly  
CC from the USPTO web site at [seqdata.uspto.gov/patseq/entry.html](http://seqdata.uspto.gov/patseq/entry.html)  
XX  
XX Sequence 104 AA;  
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ID ABU59026 standard; protein; 104 AA.  
XX AC ABU59026;  
XX DT 16-APR-2003 (first entry)  
XX DE Human secreted/transmembrane protein, #163.  
XX KW Human; PRO; secreted; transmembrane; signal peptide; pharmaceutical;  
KW diagnostic; biosensor; bioreactor; tumour; therapeutic; colon cancer;  
KW lung cancer; breast cancer; cancer; gene therapy.  
XX OS Homo sapiens.  
XX PN US2002142961-A1.  
XX PD 03-OCT-2002.  
XX PF 19-NOV-2001; 2001US-00989721.  
XX PR 16-JUN-1997; 97US-0049787P.  
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PR 25-FEB-1998; 98US-0075945P.  
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PR 07-MAY-1998; 98US-0084600P.

PR 28-MAY-1998; 98US-0087106P.  
PR 02-JUN-1998; 98US-0087607P.  
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PR 17-SEP-1998; 98WO-US019437.  
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PR 06-JAN-2000; 2000WO-US000376.  
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PR 02-MAR-2000; 2000WO-US005841.  
PR 10-MAR-2000; 2000WO-US006319.  
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PR 17-MAY-2000; 2000WO-US013705.  
PR 22-MAY-2000; 2000WO-US014042.  
PR 20-MAY-2000; 2000WO-US014941.  
PR 02-JUN-2000; 2000WO-US015264.  
PR 28-JUL-2000; 2000WO-US020710.  
PR 11-AUG-2000; 2000WO-US022031.

radiolabel; antibody; cell death; tissue typing; gene therapy;  
cytostatic; chromosome mapping; gene mapping; transgenic animal;  
knockout animal; immunohistochemical staining.

KW	radiolabel; antibody; cell death; tissue typing; gene therapy;
KW	cytostatic; chromosome mapping; gene mapping; transgenic animal;
KW	knockout animal; immunohistochemical staining.
OS	Homo sapiens.
XX	US2003022187-A1.
XX	30-JAN-2003.
XX	14-NOV-2001; 2001US-00993667.
XX	16-JUN-1997; 97US-0049787P.
XX	17-OCT-1997; 97US-0062250P.
XX	05-NOV-1997; 97WO-US020069.
XX	12-NOV-1997; 97US-0065186P.
XX	13-NOV-1997; 97US-0065311P.
XX	24-NOV-1997; 97US-0066770P.
XX	25-FEB-1998; 98US-0075945P.
XX	20-MAR-1998; 98US-0078910P.
XX	28-APR-1998; 98US-0083322P.
XX	07-MAY-1998; 98US-0084600P.
XX	28-MAY-1998; 98US-0087106P.
XX	02-JUN-1998; 98US-0087607P.
XX	02-JUN-1998; 98US-0087609P.
XX	02-JUN-1998; 98US-0087759P.
XX	03-JUN-1998; 98US-0087827P.
XX	04-JUN-1998; 98US-0088021P.
XX	04-JUN-1998; 98US-0088025P.
XX	04-JUN-1998; 98US-0088026P.
XX	04-JUN-1998; 98US-0088028P.
XX	04-JUN-1998; 98US-0088029P.
XX	04-JUN-1998; 98US-0088030P.
XX	04-JUN-1998; 98US-0088033P.
XX	04-JUN-1998; 98US-0088326P.
XX	05-JUN-1998; 98US-0088167P.
XX	05-JUN-1998; 98US-0088202P.
XX	05-JUN-1998; 98US-0088212P.
XX	05-JUN-1998; 98US-0088217P.
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XX	10-JUN-1998; 98US-0088734P.
XX	10-JUN-1998; 98US-0088738P.
XX	10-JUN-1998; 98US-0088810P.
XX	10-JUN-1998; 98US-0088824P.
XX	10-JUN-1998; 98US-0088826P.
XX	11-JUN-1998; 98US-0088858P.
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XX	12-JUN-1998; 98US-00889105P.
XX	16-JUN-1998; 98US-0089440P.
XX	16-JUN-1998; 98US-0089512P.
XX	16-JUN-1998; 98US-0089514P.
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XX	17-JUN-1998; 98US-0089599P.
XX	17-JUN-1998; 98US-0089600P.
XX	18-JUN-1998; 98US-0089653P.
XX	18-JUN-1998; 98US-0089801P.
XX	18-JUN-1998; 98US-0089907P.
XX	18-JUN-1998; 98US-0089908P.
XX	19-JUN-1998; 98US-0089947P.
XX	19-JUN-1998; 98US-0089948P.
XX	19-JUN-1998; 98US-0089952P.
XX	22-JUN-1998; 98US-0090246P.
XX	22-JUN-1998; 98US-0090252P.
XX	22-JUN-1998; 98US-0090254P.
XX	22-JUN-1998; 98US-0090282P.
XX	23-JUN-1998; 98US-0090349P.
XX	23-JUN-1998; 98US-0090355P.
XX	24-JUN-1998; 98US-0090429P.
XX	24-JUN-1998; 98US-0090431P.

23-AUG-2000; 2000WO-US023522.  
24-AUG-2000; 2000WO-US023328.  
08-NOV-2000; 2000WO-US030952.  
01-DEC-2000; 2000WO-US032678.  
28-FEB-2001; 2001WO-US006520.  
01-JUN-2001; 2001WO-US017800.  
20-JUN-2001; 2001WO-US019692.  
29-JUN-2001; 2001WO-US021066.  
09-JUL-2001; 2001WO-US021735.  
28-AUG-2001; 2001US-00941992.  
(GETH ) GENENTECH INC.  
Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Geritsen ME, Goddard A, Godowski PJ;  
Grimaldi JC, Gurney AL, Kijavini JJ, Napier MA, Pan J, Paoni NF;  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
Zhang Z;  
WPI; 2003-155950/15.  
New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,  
PRO361 or PRO846) useful as targets for therapeutic intervention in  
cancers (e.g. lung or breast cancers), or for diagnosing these cancers.  
Claim 12; Fig 290; 647pp; English.  
The invention discloses isolated PRO secreted/transmembrane polypeptides  
comprising a sequence without signal peptide and the nucleic acid  
encoding them. The polypeptides can be used to raise antibodies that  
specifically bind to the PRO polypeptide, for linking a bioactive  
molecule to a cell expressing a PRO protein and for modulating at least  
one biological activity of a cell. The PRO polypeptides or  
polynucleotides are also useful as pharmaceuticals, diagnostics,  
biosensors or bioreactors, for detecting or treating e.g. tumours in  
mammals, e.g. humans, dogs, cats, cattle, horses, sheep, goats or  
rabbits as targets for therapeutic intervention in certain cancers (e.g.  
colon, lung or breast cancers) and diagnostic determination of the  
presence of these cancers. The PRO polypeptides are also useful as  
molecular weight markers or for chromosome identification. The PRO genes  
are useful as hybridisation probes or for screening libraries of human  
cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene  
therapy, particularly for replacing a defective gene. The sequences  
presented in ABUS8900-ABUS9046 are the PRO polypeptides of the invention  
Sequence 104 AA;  
Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
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Db 1 MKLAALGLCVALSASAAFLVGSAPVAPVALESAAEAGAGTIANPLGTLNPKLL 60  
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Db 61 LSSGIPVNHIEGSKCVALGPGQAVGAVKALKALIGALTVEF 104  
RESULT 16  
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ID ABUS2404 standard; protein; 104 AA.  
XX AC ABUS2404;  
XX DT 16-JUL-2003 (first entry)  
XX DE Novel human secreted and transmembrane protein PRO1245.  
KW Human; secreted and transmembrane protein; PRO; PRO183; PRO184; PRO185;  
PRO243; PRO1133; PRO3137; PRO363; PRO5723; PRO1114; PRO3301;  
PRO9940; PRO1181; PRO7170; PRO361; PRO846; bioactive molecule; toxin;

Query Match	Score	DB	Length
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Mismatches	0	1.4e-48	0
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DB	1	MKLAALLGLCVALLSCSSAAAFVLSGAKPVAQPVAALESAAAGAGTIANPLGTLNPKLL	60
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DB	61	LSSLGIPVNHIEGSKVAELGPQAVGAVKALKALIGALTVEG	104
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XX	ABU59469;		
XX	AC		
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XX	KW	Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;	
XX	KW	cardiac insufficiency disorder; cancer; tumour; immune response;	
XX	KW	adrenal cortical capillary endothelial growth; c-fos induction;	
XX	KW	vascular endothelial growth factor inhibition; VEGF inhibition;	
XX	KW	endothelial cell growth inhibitor; T-lymphocytes stimulation;	
XX	KW	retinal neurons cell survival; rod photoreceptor cell survival;	

retinal disorder; retinitis pigmentosa; kidney disorder;  
mammalian kidney mesangial cell proliferation; Berger disease;  
maternal; herpetic formis; Crohn's disease; chondrocyte proliferation;  
chondrocyte redifferentiation; sports injury; arthritis.

KW	retinal disorder; retinitis pigmentosa; kidney disorder;	PR	24-JUN-1998;	98US-0090435P.
KW	mammalian kidney mesangial cell proliferation; Berger disease;	PR	24-JUN-1998;	98US-0090444P.
KW	maternal; herpetic formis; Crohn's disease; chondrocyte proliferation;	PR	24-JUN-1998;	98US-0090445P.
KW	chondrocyte redifferentiation; sports injury; arthritis.	PR	24-JUN-1998;	98US-0090472P.
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XX		PR	24-JUN-1998;	98US-0100634P.

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PR	17-SEP-1998;	98US-0100858P.	XX		
PR	17-SEP-1998;	98WC-US019437.	XX	20-NOV-2001;	2001US-00989724.
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Db	1	MKLAALIGLCVALSCSAAPLVGSAKPVAQPVAALSAEABAGAGTLANPLGTLNPLKLL 60			
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Db	61	LSSLGIPVNHLEIGSQKCVAEFGQAVGAVKALKALLGALTTFVG 104			
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ID	ABU92235 standard; protein; 104 AA.				
XX	AC				
XX	ABU92235;				
XX	DE				
DT	16-JUN-2003 (first entry)				
XX	DE				
XX	Novel human secreted and transmembrane protein PRO1245.				
KW	Human; secreted and transmembrane protein; PRO; neurotropic;				
KW	neuroprotective; antiparkinsonian; cytostatic; gene therapy;				
KW	chromosome mapping; gene mapping; transgenic animal; knock-out animal;				
KW	neurodegenerative disorder; Parkinson's disease; Alzheimer's disease.				
XX	Homo sapiens.				
OS	Homo sapiens.				
XX	US2003017476-A1.				
PN	XX				
XX	PR				

PR 25-JUN-1998;	98US-0090678P.	PR 02-JUN-1999;	99WO-US012252.
PR 25-JUN-1998;	98US-0090690P.	PR 23-JUN-1999;	99US-0141037P.
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PR 01-JUL-1998;	98US-0091360P.	PR 15-SEP-1999;	99WO-US021090.
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PR 17-SEP-1998;	98US-0100858P.		
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PR 07-OCT-1998;	98WO-US021141.		
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PR 08-MAR-1999;	99WO-US005028.		
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Query March 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48; Mismatches 0; Indels 0; Gaps 0;  
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OY 1 MKLAALGLCVALSAAFLVGSAPVAPVAALESAAEAGAGTANPLGLTNPLKLL 60  
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Db 1 MKLAALGLCVALSAAFLVGSAPVAPVAALESAAEAGAGTANPLGLTNPLKLL 60  
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OY 61 LSSLGIPVNHLEGSQKCVAEELGPQAVGAVKALKALLGALTVP 104  
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RESULT 19  
ABU10941  
ID ABU10941 standard; protein; 104 AA.  
XX AC ABU10941;  
XX DT 04-FEB-2003 (first entry)  
XX DE Human PRO polypeptide #127.  
XX KW Human; PRO; secreted polypeptide; transmembrane polypeptide; toxin;  
KW radiolabel; cell death; gene mapping; chromosome mapping;  
KW protein electrophoresis; genetic disorder; immunosuppressive; cytostatic;  
antibacterial.  
XX OS Homo sapiens.  
XX PN US2002123463-A1.  
XX PD 05-SEP-2002.  
XX PF 19-NOV-2001; 2001US-00989732.

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XX 16-JUN-1997; 97US-0049787P.
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PR 05-NOV-1997; 97WO-US020059.
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PR 25-FEB-1998; 98US-0075945P.
PR 20-MAR-1998; 98US-0078910P.
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PR 18-JUN-1998; 98US-0089908P.
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PR 07-OCT-1998; 98WO-US021141.
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PR 30-NOV-1999; 99WO-US028313.
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PR 24-FEB-2000; 2000WO-US005004.
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PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
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PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX (GETH ) GENENTECH INC.
PA Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
PI Grimaldi JC, Gurney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
PI Zhang Z;
XX WFI; 2003-066810/06.
DR N-PSDB; ABX17173.
XX
PT Novel secreted and transmembrane polypeptide for modulating biological
PT activity of cell expressing the polypeptide, identifying agonists or
PT antagonists of polypeptide, and as molecular weight markers.
XX
XX Claim 12; Fig 290; 655pp; English.
XX
XX The invention relates to a secreted and transmembrane polypeptide, termed
CC PRO polypeptide, and the polynucleotide encoding it. The polypeptide is
CC useful for detecting PRO polypeptides and for linking a bioactive
CC molecule to a cell expressing the above polypeptides where the bioactive
CC molecule is a toxin, radiolabel or an antibody. The bioactive material
CC causes the death of the cell. The polypeptide is useful for identifying
CC agonists or antagonists of the PRO polypeptide, for preparing variants of
CC PRO, as a molecular weight marker for protein electrophoresis purposes
CC and the PRO polynucleotide is useful for recombinantly expressing those
CC markers. The polynucleotide is also useful as a hybridisation probe, in
CC chromosome and gene mapping, in generation of antisense RNA and DNA, in
CC the preparation of PRO polypeptide, for generating transgenic animals or
CC knockout animals which in turn are useful in the development and
CC screening of therapeutically useful reagents, to construct hybridisation
CC probes for mapping the gene which encodes PRO and for the genetic
CC analysis of individuals with genetic disorders, in gene therapy, for
CC chromosome identification, as a chromosome marker and for generating
CC probes for PCR, Northern analysis, Southern analysis and Western
CC analysis. This sequence represents a human PRO polypeptide of the
CC invention
XX
XX Sequence 104 AA;
Query Match 100.0%; Score 502; DB 6; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MKLAALLGLCVALSCTSSAAAFVLSAKFVAQPVAALESAAEAGAGTLANPLGTLNPKLL 60
DB 1 MKLAALLGLCVALSCTSSAAAFVLSAKFVAQPVAALESAAEAGAGTLANPLGTLNPKLL 60
QY 61 LSSLGIPVNHLEIGSQKCVBELGPOAVGKALKALIGALTIVFG 104
DB 61 LSSLGIPVNHLEIGSQKCVBELGPOAVGKALKALIGALTIVFG 104
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	PR	18-JUN-1986;	98US-U089801P.	
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	PR	18-JUN-1986;	98US-U089908P.	
	PR	16-SEP-1986;	98WO-US019330.	
	PR	17-SEP-1986;	98WO-US019437.	
	PR	17-OCT-1986;	98WO-US021141.	
	PR	01-DEC-1986;	98WO-US025108.	
	PR	05-JAN-1989;	99WO-US000106.	
	PR	08-MAR-1989;	99WO-US005028.	
	PR	02-JUN-1989;	99WO-US012252.	
	PR	15-SEP-1989;	99WO-US021090.	
	PR	15-SEP-1989;	99WO-US021547.	
	PR	30-NOV-1989;	99WO-US028313.	
	PR	01-DEC-1989;	99WO-US028301.	
	PR	01-DEC-1989;	99WO-US028634.	
	PR	16-DEC-1989;	99WO-US030095.	
	PR	20-DEC-1989;	99WO-US030911.	
	PR	05-JAN-2000;	2000WO-US000219.	
	PR	11-FEB-2000;	2000WO-US000376.	
	PR	11-FEB-2000;	2000WO-US003565.	
	PR	18-FEB-2000;	2000WO-US004341.	
	PR	22-FEB-2000;	2000WO-US004414.	
	PR	24-FEB-2000;	2000WO-US004914.	
	PR	02-MAR-2000;	2000WO-US005004.	
	PR	10-MAR-2000;	2000WO-US005841.	
	PR	15-MAR-2000;	2000WO-US006319.	
	PR	20-MAR-2000;	2000WO-US006884.	
	PR	30-MAR-2000;	2000WO-US007377.	
	PR	15-MAY-2000;	2000WO-US013358.	
	PR	22-MAY-2000;	2000WO-US013705.	
	PR	30-MAY-2000;	2000WO-US014042.	
	PR	02-JUN-2000;	2000WO-US014941.	
	PR	28-JUL-2000;	2000WO-US015264.	
	PR	11-AUG-2000;	2000WO-US020710.	
	PR	23-AUG-2000;	2000WO-US022031.	
	PR	24-AUG-2000;	2000WO-US023522.	
	PR	08-NOV-2000;	2000WO-US023328.	
	PR	01-DEC-2000;	2000WO-US030952.	
	PR	28-FEB-2001;	2001WO-US006520.	
	PR	01-JUN-2001;	2001WO-US017800.	
	PR	20-JUN-2001;	2001WO-US019692.	
	PR	29-JUN-2001;	2001WO-US021066.	
	PR	03-JUL-2001;	2001WO-US021735.	
	PR	28-AUG-2001;	2001US-U0941992.	
	XX	(GETH ) GENENTECH INC.		
	PA	Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL; Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Gcdowski PJ; Grimaldi JC, Gurney AL, KJlavin IJ, Napier MA, Pan J, Paoni NF; Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI; Zhang Z;		
	XX	WFI; 2003-328481/31.		
	DR	N-PSDB; ACA68028.		
	XX	New secreted and transmembrane polypeptide, useful for modulating biological activity of cell expressing the polypeptide, for identifying agonists or antagonists of polypeptide, and as molecular weight markers.		
	PT	Claim 12; Fig 290; 654pp; English.		
	ES	The invention describes an isolated, secreted and transmembrane polypeptide (I), termed PRO polypeptide. (II) is useful for detecting PRO943, PRO183, PRO184, PRO185, PRO331, PRO1133, PRO363, PRO5723, PRO1387, PRO1114, PRO3940, PRO1181, PRO1170, PRO361 or PRO846 polypeptide comprising contacting the sample with the polypeptide and determining formation of a polypeptide conjugate. (I) is also useful for linking a bioactive molecule e.g. toxin, radiolabel or antibody, to a cell expressing the above polypeptides to cause cell death. (I) is also		
DE	OS	Homo sapiens.		
PN	PN	US2002177164-A1.		
PD	PD	28-NOV-2002.		
XX	PF	20-NOV-2001; 2001USU-00989293.		
XX	PP	16-JUN-1997; 97US-0049787P.		
PR	PR	17-OCT-1997; 97US-0062250P.		
PR	PR	05-NOV-1997; 97WO-US020069.		
PR	PR	12-NOV-1997; 97US-0065186P.		
PR	PR	13-NOV-1997; 97US-0065311P.		
PR	PR	24-NOV-1997; 97US-0068770P.		
PR	PR	25-FEB-1998; 98US-0075945P.		
PR	PR	20-MAR-1998; 98US-0078910P.		
PR	PR	28-APR-1998; 98US-0083322P.		
PR	PR	07-MAY-1998; 98US-0084600P.		
PR	PR	28-MAY-1998; 98US-0087106P.		
PR	PR	02-JUN-1998; 98US-0087607P.		
PR	PR	02-JUN-1998; 98US-0087603P.		
PR	PR	02-JUN-1998; 98US-0087759P.		
PR	PR	03-JUN-1998; 98US-0087827P.		
PR	PR	04-JUN-1998; 98US-0088021P.		
PR	PR	04-JUN-1998; 98US-0088025P.		
PR	PR	04-JUN-1998; 98US-0088026P.		
PR	PR	04-JUN-1998; 98US-0088028P.		
PR	PR	04-JUN-1998; 98US-0088029P.		
PR	PR	04-JUN-1998; 98US-0088030P.		
PR	PR	04-JUN-1998; 98US-0088033P.		
PR	PR	05-JUN-1998; 98US-0088326P.		

CC useful as a therapeutic agent e.g. for treating cancer and autoimmune  
CC disease. PRO is useful in assays to identify other proteins or molecules  
CC involved in binding interactions. The polynucleotide (ii) encoding (i) is  
CC useful in chromosome and gene mapping, for generating transgenic animals  
CC or knockout animals which in turn are useful in the development and  
CC screening of therapeutically useful reagents, for the genetic analysis of  
CC individuals with genetic disorders, in gene therapy, for chromosome  
CC identification, and as a chromosome marker. An anti-(i)-antibody is  
CC useful in diagnostic assays for PRO, e.g. detecting its expression in  
CC specific cells, tissues or serum, for affinity purification of PRO, and  
CC for treating septic shock. This is the amino acid sequence of a novel  
CC human secreted and transmembrane PRO polypeptide

XX  
SQ Sequence 104 AA;

Query Match 100.0%; Score 502; DB 6; Length 104;  
Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MKLALLGLCVALSCTSAARFVGSAPVQVVALESAAEAGAGTIANPLGTINPKLL 60  
DB 1 MKLALLGLCVALSCTSAARFVGSAPVQVVALESAAEAGAGTIANPLGTINPKLL 60  
OY 61 LSSLGIPVNHILIEGSKVVAELGPOAVGAVKALKALGALTVFG 104  
DB 61 LSSLGIPVNHILIEGSKVVAELGPOAVGAVKALKALGALTVFG 104

RESULT 21  
ABU88632  
ID ABU88632 standard; protein; 104 AA.

AC ABU88632;  
XX  
XX  
DT 11-AUG-2003 (first entry)  
DE Human secreted and transmembrane polypeptide PRO1245.  
XX Human; gene therapy; cancer; retinal disorder; wound healing;  
KW kidney disorder.

XX Homo sapiens.

XX US2002197615-A1.

PN 26-DEC-2002.

XX 16-NOV-2001; 2001US-00991181.

XX 16-JUN-1997; 97US-0049787P.  
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PR 04-JUN-1998; 98US-0088025P.  
PR 04-JUN-1998; 98US-0088026P.  
PR 04-JUN-1998; 98US-0088028P.  
PR 04-JUN-1998; 98US-0088029P.  
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PR 20-JUN-2001; 2001WO-US019692.  
PR 23-JUN-2001; 2001WO-US021066.  
PR 09-JUL-2001; 2001WO-US021735.  
PR 28-AUG-2001; 2001US-00941992.  
XX  
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PR 28-APR-1998; 98US-0083322P.
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PR 02-JUN-1998; 98US-0087759P.
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PR 04-JUN-1998; 98US-0088026P.
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PR 17-JUN-1998; 98US-0089599P.
PR 17-JUN-1998; 98US-0089600P.
PR 17-JUN-1998; 98US-0089633P.
PR 18-JUN-1998; 98US-0089801P.
PR 18-JUN-1998; 98US-0089907P.
PR 18-JUN-1998; 98US-0089908P.
PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 05-JAN-1999; 98WO-US000106.
PR 08-MAR-1999; 98WO-US005028.
PR 02-JUN-1999; 98WO-US012252.
PR 15-SEP-1999; 98WO-US021090.
PR 15-SEP-1999; 98WO-US021547.
PR 30-NOV-1999; 98WO-US028313.
PR 01-DEC-1999; 98WO-US028301.
PR 01-DEC-1999; 98WO-US028334.
PR 16-DEC-1999; 98WO-US030095.
PR 20-DEC-1999; 98WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 02-MAR-2000; 2000WO-US005004.
PR 10-MAR-2000; 2000WO-US005319.
PR 15-MAR-2000; 2000WO-US006884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 01-NOV-2000; 2000WO-US030952.
PR 01-DEC-2000; 2000WO-US032678.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
PR 29-JUN-2001; 2001WO-US021066.
PR 09-JUL-2001; 2001WO-US021735.
PR 28-AUG-2001; 2001US-00941992.
XX
XX (GETH ) GENENTECH INC.
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
PI Perrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ,
PI Grimaldi JC, Gurney AL, Kijavini LJ, Napier MA, Pan J, Paoi NF,
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
PI Zhang Z;
XX
XX WPI; 2003-531419/50.
XX N-PSDB; ADA37918.
XX
XX New isolated PRO183, PRO184, PRO361 or PRO845 nucleic acid and secreted
PT transmembrane polypeptides, useful as targets for the diagnosis and
PT treatment of cancers, such as lung and breast cancers.
XX
XX Claim 12; Fig 290; 660pp; English.
XX
XX The invention relates to an isolated nucleic acid molecule comprising the
CC full-length coding sequence of the DNA ATCC Accession Numbers given in
CC the specification, or comprising a sequence with at least 80% identity
CC to: (a) a nucleotide encoding any of 147 PRO polypeptides, or an
CC extracellular domain of the polypeptide; or (b) any of 147 nucleotide
CC sequences fully defined in the specification. Also included are the PRO
CC proteins (or their extracellular domains with or without their associated
CC extracellular domains), expression vectors, host cells, PRO chimeric
CC proteins, anti-PRO antibodies, methods of detecting polypeptide in a
CC sample, methods of linking a bioactive molecule to a cell expressing a
CC polypeptide and methods of modulating at least one biological activity of
CC a cell expressing the polypeptide. The PRO polypeptides or
CC polynucleotides are useful as pharmaceuticals, diagnostics, biosensors or
CC bioreactors. These are useful for stimulating hypertrophy of neonatal
CC heart, promoting angiogenesis, inhibiting vascular endothelial growth
CC factor (VEGF)-stimulated proliferation of endothelial cells, modulating
CC the proliferation of stimulated T-lymphocytes, enhancing the survival or
CC proliferation of retinal neurons or rod photoreceptor cells, inducing c-
CC fos in endothelial cells, modulating glucose or FFA uptake by adipocyte
CC cells, inducing proliferation and/or re-differentiation of chondrocytes,
CC or inducing pancreatic beta-cell precursor differentiation. In
CC particular, these are useful for detecting or treating tumours and
CC certain cancers (colon, lung or breast cancers) in mammals, e.g. humans,
CC dogs, cats, cattle, horses, sheep, pigs, goats, or rabbits. The PRO genes
CC may also be used in gene therapy, particularly for replacing a defective
CC gene. The present sequence represents a PRO protein.
XX
XX Sequence 104 AA;
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XX Query Match 100.0%; Score 502; DB 6; Length 104;
XX Best Local Similarity 100.0%; Pred. No. 1.4e-48;
XX Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 LSSIGIPVNHLEIGSKCVAEIGPQAVGAVKALKALLGALTVFG 104
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RESULT 24  
ADA21605  
ID ADA21605 standard; protein; 104 AA.  
XX AC ADA21605;  
XX DT 20-NOV-2003 (first entry)  
XX DE  
XX DE Human secreted/transmembrane polypeptide PRO1245.  
XX KW human; tumour; cancer; colorectal cancer; gene therapy;  
XX KW chondrocyte differentiation; VEGF inhibition;  
XX KW vascular endothelial growth factor; Alzheimer's disease;  
XX KW Parkinson's disease; atherosclerosis; cystic fibrosis;  
XX KW multiple sclerosis; ovarian cancer; tissue typing.  
XX OS Homo sapiens.  
XX PN US2003054404-A1.  
XX PD 20-MAR-2003.  
XX PF 15-NOV-2001; 2001US-00997601.  
XX PR 16-JUN-1997; 97US-0049787P.  
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XX PR 24-NOV-1997; 97US-0066770P.  
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RESULT 25  
ADA10392

ID ADA10392 standard; protein; 104 AA.  
XX AC ADA10392;  
XX DT 06-NOV-2003 (first entry)  
XX DE Human secreted/transmembrane protein, PRO1245.  
XX KW PRO; secreted protein; transmembrane protein; human; septic shock; immunogen.  
XX OS Homo sapiens.  
XX FN US2003059831-A1.  
XX PD 27-MAR-2003.  
XX PF 19-NOV-2001; 2001US-00989729.  
XX PR 16-JUN-1997; 97US-0049787P.  
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PR 20-MAR-1998; 98US-0078910P.  
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PR 07-MAY-1998; 98US-0084600P.  
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XX 20-NOV-2003 (first entry)  
DT Human PRO1245 polypeptide.  
XX Human; PRO polypeptide; secreted protein; transmembrane protein;  
KW transgenic; tumour; cytostatic.  
XX Homo sapiens.  
OS US2003054987-A1.  
PN 20-MAR-2003.  
PD 14-NOV-2001; 2001US-00990443.  
PF 16-JUN-1997; 97US-0049787P.  
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PR 28-APR-1998; 98US-0078910P.  
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KW hypertrophy of neonatal heart; angiogenesis;  
KW vascular endothelial growth factor; VEGF-stimulated proliferation;  
KW endothelial cell; T-lymphocyte proliferation; retinal neuron;  
KW c-fos induction; adipocyte cell; chondrocyte differentiation;  
KW pancreatic beta-cell precursor differentiation; gene therapy; tumour;  
KW cancer; human; colon cancer; lung cancer; breast cancer;  
KW rod photoreceptor cell.  
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XX Homo sapiens.  
XX  
XX OS  
XX  
XX US2003059832-A1.  
XX  
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XX PF  
XX PF  
XX XX  
XX 27-MAR-2003.  
XX 15-NOV-2001; 2001US-00997349.  
XX 16-JUN-1997; 97US-0049787P.  
XX 17-OCT-1997; 97US-0062250P.  
XX 05-NOV-1997; 97WO-0020069.  
XX 12-NOV-1997; 97US-0065186P.  
XX 13-NOV-1997; 97US-0065311P.  
XX 24-NOV-1997; 97US-0066770P.  
XX 25-FEB-1998; 98US-0075945P.  
XX 20-MAR-1998; 98US-0078910P.  
XX 28-APR-1998; 98US-0083322P.  
XX 07-MAY-1998; 98US-0084600P.  
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XX 03-JUN-1998; 98US-0087827P.  
XX 04-JUN-1998; 98US-0088021P.  
XX 04-JUN-1998; 98US-0088025P.  
XX 04-JUN-1998; 98US-0088028P.  
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XX 09-JUN-1998; 98US-0088655P.  
XX 10-JUN-1998; 98US-0088734P.  
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XX 22-JUN-1998; 98US-0090246P.  
XX 22-JUN-1998; 98US-0090252P.  
XX 22-JUN-1998; 98US-0090254P.  
XX 23-JUN-1998; 98US-0090349P.  
PR 23-JUN-1998; 98US-0090355P.  
PR 24-JUN-1998; 98US-0090429P.  
PR 24-JUN-1998; 98US-0090431P.  
PR 24-JUN-1998; 98US-0090435P.  
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PR 25-JUN-1998; 98US-0090696P.  
PR 25-JUN-1998; 98US-0090696P.  
PR 26-JUN-1998; 98US-0090862P.  
PR 26-JUN-1998; 98US-0090863P.  
PR 01-JUL-1998; 98US-0091360P.  
PR 01-JUL-1998; 98US-0091544P.  
PR 02-JUL-1998; 98US-0091478P.  
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PR 02-JUL-1998; 98US-0091633P.  
PR 02-JUL-1998; 98US-0091646P.  
PR 02-JUL-1998; 98US-0091673P.  
PR 07-JUL-1998; 98US-0091978P.  
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PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
PR 04-AUG-1998; 98US-0095285P.  
PR 04-AUG-1998; 98US-0095301P.  
PR 04-AUG-1998; 98US-0095302P.  
PR 04-AUG-1998; 98US-0095318P.  
PR 04-AUG-1998; 98US-0095321P.  
PR 04-AUG-1998; 98US-0095325P.  
PR 10-AUG-1998; 98US-0095916P.  
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PR 11-AUG-1998; 98US-0096143P.  
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PR 20-AUG-1998; 98US-0097218P.  
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PR 26-AUG-1998; 98US-0097952P.  
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PR 26-AUG-1998; 98US-0097979P.  
PR 26-AUG-1998; 98US-0097986P.  
PR 26-AUG-1998; 98US-0097988P.

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PR	17-SEP-1998;	98US-0100858P.	XX	
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PR	22-DEC-1998;	98US-0113296P.	PR	17-OCT-1997; 97US-0062250P.
PR	05-JAN-1999;	99WO-US000106.	PR	05-NOV-1997; 97WO-US020069.
PR	08-MAR-1999;	99WO-US005028.	PR	12-NOV-1997; 97US-0065186P.
PR	12-MAR-1999;	99US-0123957P.	PR	13-NOV-1997; 97US-0065311P.
PR	02-JUN-1999;	99WO-US012252.	PR	25-NOV-1997; 97US-0066770P.
PR	23-JUN-1999;	99US-0141037P.	PR	25-FEB-1998; 98US-0075945P.
PR	07-JUL-1999;	99US-0143048P.	PR	20-MAR-1998; 98US-0078910P.
PR	20-JUL-1999;	99US-0144758P.	PR	28-APR-1998; 98US-0083322P.
PR	26-JUL-1999;	99US-0145698P.	PR	07-MAY-1998; 98US-0084600P.
PR	28-JUL-1999;	99US-0146222P.	PR	28-MAY-1998; 98US-0087106P.
PR	17-AUG-1999;	99US-0149396P.	PR	02-JUN-1998; 98US-0087609P.
PR	15-SEP-1999;	99WO-US021090.	PR	02-JUN-1998; 98US-0087759P.
PR	15-SEP-1999;	99WO-US021547.	PR	02-JUN-1998; 98US-0087827P.
PR	08-OCT-1999;	99US-0158663P.	PR	03-JUN-1998; 98US-0088021P.
PR	30-NOV-1999;	99WO-US028313.	PR	04-JUN-1998; 98US-0088025P.
PR	01-DEC-1999;	99WO-US028301.	PR	04-JUN-1998; 98US-0088026P.
PR	16-DEC-1999;	99WO-US030095.	PR	04-JUN-1998; 98US-0088028P.
PR	20-DEC-1999;	99WO-US030311.	PR	04-JUN-1998; 98US-0088029P.
PR	05-JAN-2000;	2000WO-US000219.	PR	04-JUN-1998; 98US-0088030P.
PR	06-JAN-2000;	2000WO-US000376.	PR	04-JUN-1998; 98US-0088033P.
PR	11-FEB-2000;	2000WO-US003565.	PR	04-JUN-1998; 98US-0088326P.
PR	18-FEB-2000;	2000WO-US004341.	PR	05-JUN-1998; 98US-0088467P.
PR	22-FEB-2000;	2000WO-US004414.	PR	05-JUN-1998; 98US-0088202P.
PR	24-FEB-2000;	2000WO-US004914.	PR	05-JUN-1998; 98US-0088212P.
PR	02-MAR-2000;	2000WO-US005004.	PR	09-JUN-1998; 98US-0088655P.
PR	02-MAR-2000;	2000WO-US005841.	PR	10-JUN-1998; 98US-0088734P.
PR	10-MAR-2000;	2000WO-US006319.	PR	10-JUN-1998; 98US-0088738P.
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PR	20-MAR-2000;	2000WO-US007377.	PR	10-JUN-1998; 98US-0088810P.
PR	30-MAR-2000;	2000WO-US008439.	PR	10-JUN-1998; 98US-0088824P.
PR	15-MAY-2000;	2000WO-US013358.	PR	10-JUN-1998; 98US-0088826P.
PR	17-MAY-2000;	2000WO-US013705.	PR	11-JUN-1998; 98US-0088858P.
PR	22-MAY-2000;	2000WO-US014042.	PR	11-JUN-1998; 98US-0088861P.
PR	30-MAY-2000;	2000WO-US014941.	PR	11-JUN-1998; 98US-0088876P.
PR	02-JUN-2000;	2000WO-US015264.	PR	12-JUN-1998; 98US-0089105P.
PR	23-JUN-2000;	2000US-0213637P.	PR	16-JUN-1998; 98US-0089440P.
Query Match 100.0%; Score 502; DB 6; Length 104;				
Best Local Similarity 100.0%; Pred No. 1.4e-48;				
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Db	1	MKLAALLGLCVALLSCSSAAFLVGSAPVQPVAALESAAEAGAGTLANPLGTINPLKLL 60		
QY	61	LSSLGIPVNHLEGSQKVAELGPQAVGAVKALKALIGALTVEG 104		
Db	61	LSSLGIPVNHLEGSQKVAELGPQAVGAVKALKALIGALTVEG 104		
RESULT 29				
ID	ADA38849			
XX	ADA38849	standard; protein; 104 AA.		
AC	ADA38849;			
XX	ADA38849;			
DT	20-NOV-2003.	(first entry)		
XX	Human secreted/transmembrane protein PRO1245.			
DE	PRO; secreted protein; transmembrane protein; gene therapy; tumour;			
XX	cancer; human; colon cancer; lung cancer; breast cancer.			
KW	Homo sapiens.			
XX				
OS				

PR	24-JUN-1998;	98US-0090542P.	PR	05-JAN-1999;	99WO-US000106.
PR	24-JUN-1998;	98US-0090557P.	PR	08-MAR-1999;	99WO-US005028.
PR	25-JUN-1998;	98US-0090676P.	PR	12-MAR-1999;	99US-0123557P.
PR	25-JUN-1998;	98US-0090678P.	PR	02-JUN-1999;	99WO-US012252.
PR	25-JUN-1998;	98US-0090690P.	PR	23-JUN-1999;	99US-0141037P.
PR	25-JUN-1998;	98US-0090694P.	PR	07-JUL-1999;	99US-0143048P.
PR	25-JUN-1998;	98US-0090695P.	PR	20-JUL-1999;	99US-0144758P.
PR	25-JUN-1998;	98US-0090696P.	PR	26-JUL-1999;	99US-0145698P.
PR	25-JUN-1998;	98US-0090862P.	PR	28-JUL-1999;	99US-0146222P.
PR	26-JUN-1998;	98US-0090863P.	PR	17-AUG-1999;	99US-0149396P.
PR	26-JUN-1998;	98US-0090863P.	PR	15-SEP-1999;	99WO-US021090.
PR	01-JUL-1998;	98US-0091360P.	PR	15-SEP-1999;	99WO-US021547.
PR	01-JUL-1998;	98US-0091544P.	PR	08-OCT-1999;	99US-0158663P.
PR	02-JUL-1998;	98US-0091478P.	PR	30-NOV-1999;	99WO-US028313.
PR	02-JUL-1998;	98US-0091519P.	PR	01-DEC-1999;	99WO-US028301.
PR	02-JUL-1998;	98US-0091626P.	PR	01-DEC-1999;	99WO-US028634.
PR	02-JUL-1998;	98US-0091628P.	PR	16-DEC-1999;	99WO-US030095.
PR	02-JUL-1998;	98US-0091633P.	PR	20-DEC-1999;	99WO-US030311.
PR	02-JUL-1998;	98US-0091646P.	PR	05-JAN-2000;	2000WO-US000219.
PR	02-JUL-1998;	98US-0091673P.	PR	06-JAN-2000;	2000WO-US000376.
PR	07-JUL-1998;	98US-0091978P.	PR	11-FEB-2000;	2000WO-US003565.
PR	07-JUL-1998;	98US-0091982P.	PR	18-FEB-2000;	2000WO-US004341.
PR	09-JUL-1998;	98US-0092182P.	PR	22-FEB-2000;	2000WO-US004414.
PR	10-JUL-1998;	98US-0092472P.	PR	24-FEB-2000;	2000WO-US004914.
PR	30-JUL-1998;	98US-0093339P.	PR	24-FEB-2000;	2000WO-US005004.
PR	04-AUG-1998;	98US-0094651P.	PR	02-MAR-2000;	2000WO-US005841.
PR	04-AUG-1998;	98US-0095282P.	PR	10-MAR-2000;	2000WO-US006319.
PR	04-AUG-1998;	98US-0095304P.	PR	15-MAR-2000;	2000WO-US006884.
PR	04-AUG-1998;	98US-0095318P.	PR	20-MAR-2000;	2000WO-US007377.
PR	04-AUG-1998;	98US-0095321P.	PR	30-MAR-2000;	2000WO-US008439.
PR	04-AUG-1998;	98US-0095325P.	PR	15-MAY-2000;	2000WO-US013358.
PR	10-AUG-1998;	98US-0095916P.	PR	17-MAY-2000;	2000WO-US013705.
PR	10-AUG-1998;	98US-0095929P.	PR	22-MAY-2000;	2000WO-US014042.
PR	10-AUG-1998;	98US-0096012P.	PR	30-MAY-2000;	2000WO-US014941.
PR	10-AUG-1998;	98US-0096143P.	PR	02-JUN-2000;	2000WO-US015264.
PR	11-AUG-1998;	98US-0096146P.	PR	23-JUN-2000;	2000US-0213637P.
PR	12-AUG-1998;	98US-0096329P.	PR	28-JUL-2000;	2000WO-US020710.
PR	17-AUG-1998;	98US-0096757P.	PR	11-AUG-2000;	2000WO-US022031.
PR	17-AUG-1998;	98US-0096766P.	PR	23-AUG-2000;	2000WO-US023522.
PR	17-AUG-1998;	98US-0096768P.	PR	24-AUG-2000;	2000WO-US023328.
PR	17-AUG-1998;	98US-0096773P.	PR	07-SEP-2000;	2000US-0230978P.
PR	17-AUG-1998;	98US-0096791P.	PR	08-NOV-2000;	2000WO-US030952.
PR	17-AUG-1998;	98US-0096867P.			
PR	17-AUG-1998;	98US-0096891P.			
PR	17-AUG-1998;	98US-0096894P.			
PR	17-AUG-1998;	98US-0096895P.			
PR	17-AUG-1998;	98US-0096897P.			
PR	18-AUG-1998;	98US-0096930P.			
PR	18-AUG-1998;	98US-0096959P.			
PR	18-AUG-1998;	98US-0096960P.			
PR	18-AUG-1998;	98US-0097022P.			
PR	19-AUG-1998;	98US-0097141P.			
PR	20-AUG-1998;	98US-0097218P.			
PR	24-AUG-1998;	98US-0097661P.			
PR	26-AUG-1998;	98US-0097952P.			
PR	26-AUG-1998;	98US-0097954P.			
PR	26-AUG-1998;	98US-0097955P.			
PR	26-AUG-1998;	98US-0097971P.			
PR	26-AUG-1998;	98US-0097974P.			
PR	26-AUG-1998;	98US-0097978P.			
PR	26-AUG-1998;	98US-0097979P.			
PR	26-AUG-1998;	98US-0097986P.			
PR	26-AUG-1998;	98US-0098014P.			
PR	31-SEP-1998;	98US-0098525P.			
PR	16-SEP-1998;	98US-0100634P.			
PR	16-SEP-1998;	98WO-US019330.			
PR	17-SEP-1998;	98WO-US019437.			
PR	17-SEP-1998;	98WO-US021141.			
PR	01-OCT-1998;	98WO-US025108.			
PR	22-DEC-1998;	98US-0113296P.			
			Query Match 100.0%; Score 502; DB 6; Length 104;		
			Best Local Similarity 100.0%; Pred. No. 1.4e-48;		
			Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;		
QY	1	MKLAALLGLCVALS	QY	1	MKLAALLGLCVALS
DB	1	MKLAALLGLCVALS	DB	1	MKLAALLGLCVALS
QY	61	LSSLGIPVNHLEGSQKVAELGPOAVGAVKALCALTVFG	QY	61	LSSLGIPVNHLEGSQKVAELGPOAVGAVKALCALTVFG
DB	61	LSSLGIPVNHLEGSQKVAELGPOAVGAVKALCALTVFG	DB	61	LSSLGIPVNHLEGSQKVAELGPOAVGAVKALCALTVFG
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ADA92970					
ID	ADA92970 standard; protein; 104 AA.				
XX	ADA92970;				
XX	20-NOV-2003 (first entry)				
XX	Human secreted/transmembrane protein PRO1245.				
XX	PRO; secreted protein; transmembrane protein;				
XX	hyper trophy of neonatal heart; angiogenesis;				
XX	vascular endothelial growth factor; VEGF-stimulated proliferation;				
XX	endothelial cell; T-lymphocyte proliferation; retinal neuron;				
XX	c-fos induction; adipocyte cell; chondrocyte differentiation;				
XX	pancreatic beta-cell precursor differentiation; gene therapy; tumour;				
XX	cancer; human; colon cancer; lung cancer; breast cancer;				



PR	07-OCT-1998;	98WO-US021141.	PR	07-OCT-1998;	98WO-US021141.
PR	01-DEC-1998;	98WO-US025108.	PR	01-DEC-1998;	98WO-US025108.
PR	22-DEC-1998;	98US-0113298P.	PR	22-DEC-1998;	98US-0113298P.
PR	05-JAN-1999;	98WO-US000106.	PR	05-JAN-1999;	98WO-US000106.
PR	08-MAR-1999;	98WO-US005028.	PR	08-MAR-1999;	98WO-US005028.
PR	12-MAR-1999;	98US-0123957P.	PR	12-MAR-1999;	98US-0123957P.
PR	02-JUN-1999;	98WO-US012252.	PR	02-JUN-1999;	98WO-US012252.
PR	23-JUN-1999;	98US-0141037P.	PR	23-JUN-1999;	98US-0141037P.
PR	07-JUL-1999;	98US-0143048P.	PR	07-JUL-1999;	98US-0143048P.
PR	20-JUL-1999;	98US-0144758P.	PR	20-JUL-1999;	98US-0144758P.
PR	26-JUL-1999;	98US-0145698P.	PR	26-JUL-1999;	98US-0145698P.
PR	28-JUL-1999;	98US-0146222P.	PR	28-JUL-1999;	98US-0146222P.
PR	17-AUG-1999;	98US-0149396P.	PR	17-AUG-1999;	98US-0149396P.
PR	15-SEP-1999;	98WO-US021090.	PR	15-SEP-1999;	98WO-US021090.
PR	08-OCT-1999;	98US-0158663P.	PR	08-OCT-1999;	98US-0158663P.
PR	15-SEP-1999;	98WO-US021547.	PR	15-SEP-1999;	98WO-US021547.
PR	30-NOV-1999;	98US-0158663P.	PR	30-NOV-1999;	98US-0158663P.
PR	01-DEC-1999;	98WO-US028313.	PR	01-DEC-1999;	98WO-US028313.
PR	01-DEC-1999;	98WO-US028634.	PR	01-DEC-1999;	98WO-US028634.
PR	16-DEC-1999;	98WO-US030095.	PR	16-DEC-1999;	98WO-US030095.
PR	20-DEC-1999;	98WO-US030911.	PR	20-DEC-1999;	98WO-US030911.
PR	05-JAN-2000;	2000WO-US000219.	PR	05-JAN-2000;	2000WO-US000219.
PR	11-FEB-2000;	2000WO-US000376.	PR	11-FEB-2000;	2000WO-US000376.
PR	18-FEB-2000;	2000WO-US003565.	PR	18-FEB-2000;	2000WO-US003565.
PR	22-FEB-2000;	2000WO-US004411.	PR	22-FEB-2000;	2000WO-US004411.
PR	24-FEB-2000;	2000WO-US004914.	PR	24-FEB-2000;	2000WO-US004914.
PR	24-FEB-2000;	2000WO-US005004.	PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.	PR	02-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.	PR	10-MAR-2000;	2000WO-US006319.
PR	15-MAR-2000;	2000WO-US006884.	PR	15-MAR-2000;	2000WO-US006884.
PR	20-MAR-2000;	2000WO-US007377.	PR	20-MAR-2000;	2000WO-US007377.
PR	30-MAR-2000;	2000WO-US008439.	PR	30-MAR-2000;	2000WO-US008439.
PR	15-MAY-2000;	2000WO-US013358.	PR	15-MAY-2000;	2000WO-US013358.
PR	22-MAY-2000;	2000WO-US014042.	PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.	PR	30-MAY-2000;	2000WO-US014941.
PR	02-JUN-2000;	2000WO-US015264.	PR	02-JUN-2000;	2000WO-US015264.
PR	23-JUN-2000;	2000US-0213637P.	PR	23-JUN-2000;	2000US-0213637P.
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Best Local Similarity 100.0%; Pred. No. 1.4e-46;					
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Db	1	MKLAALLGLCVALLSCSSAAFLVGSAPVQVAALESAAAGACTLANPLGTINPLKLL	60		
Qy	61	LSSLGIPVNHLEGSQKVAELGPQAVGAVKALKALLGALTVEG	104		
Db	61	LSSLGIPVNHLEGSQKVAELGPQAVGAVKALKALLGALTVEG	104		
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XX	AC ABO53232;				
XX	14-OCT-2003 (first entry)				
DT	Human secreted/transmembrane protein PRO1245.				
DE	Human; secreted protein; transmembrane protein; PRO;				
KW	adrenal cortical capillary endothelial cell; angiogenesis; wound healing;				
KW	diabetes; obesity; hyper-insulinaemia; hypo-insulinaemia;				
KW	chondrocyte redifferentiation; bone disorder; cartilage disorder;				
KW	sports injury; arthritis; kidney mesangial cell proliferation;				
KW	kidney disorder; Berger disease; neuropathy; coeliac disease;				
KW	dermatitis herpetiformis; Crohn's disease; tumour; cancer.				
OS	Homo sapiens.				
XX					

US2003044806-A1.

06-MAR-2003.

15-NOV-2001; 2001US-00998156.

16-JUN-1997; 97US-0049787P.  
17-OCT-1997; 97US-0062250P.  
05-NOV-1997; 97WO-US020069.  
12-NOV-1997; 97US-0065186P.  
13-NOV-1997; 97US-0065311P.  
24-NOV-1997; 97US-0066770P.  
25-FEB-1998; 98US-0075945P.  
20-MAR-1998; 98US-0078910P.  
28-APR-1998; 98US-0083322P.  
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02-JUN-1998; 98US-0087607P.  
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PR 10-JUL-1998; 98US-0092472P.
PR 20-JUL-1998; 98US-0093339P.
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PR 11-AUG-1998; 98US-0096146P.
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PR 26-AUG-1998; 98US-0098014P.
PR 31-AUG-1998; 98US-0098525P.
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PR 16-SEP-1998; 98WO-US019330.
PR 17-SEP-1998; 98US-0100858P.
PR 17-SEP-1998; 98WO-US019437.
PR 07-OCT-1998; 98WO-US021141.
PR 01-DEC-1998; 98WO-US025108.
PR 22-DEC-1998; 98US-0113296P.
PR 05-JAN-1999; 99WO-US000106.

PR 08-MAR-1999; 99WO-US0005028.
PR 12-MAR-1999; 99US-0123957P.
PR 02-JUN-1999; 99WO-US012252.
PR 23-JUN-1999; 99US-0141037P.
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PR 28-JUL-1999; 99US-0146222P.
PR 17-AUG-1999; 99US-0149396P.
PR 15-SEP-1999; 99WO-US021090.
PR 15-SEP-1999; 99WO-US021547.
PR 08-OCT-1999; 99US-0158663P.
PR 30-NOV-1999; 99WO-US028313.
PR 01-DEC-1999; 99WO-US028301.
PR 16-DEC-1999; 99WO-US028634.
PR 20-DEC-1999; 99WO-US030095.
PR 20-DEC-1999; 99WO-US030911.
PR 05-JAN-2000; 2000WO-US000219.
PR 06-JAN-2000; 2000WO-US000376.
PR 11-FEB-2000; 2000WO-US003565.
PR 18-FEB-2000; 2000WO-US004341.
PR 22-FEB-2000; 2000WO-US004414.
PR 24-FEB-2000; 2000WO-US004914.
PR 02-MAR-2000; 2000WO-US005841.
PR 10-MAR-2000; 2000WO-US006319.
PR 15-MAR-2000; 2000WO-US008884.
PR 20-MAR-2000; 2000WO-US007377.
PR 30-MAR-2000; 2000WO-US008439.
PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
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PR 30-MAY-2000; 2000WO-US014941.
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PR 28-JUL-2000; 2000WO-US020710.

Query Match 100.0%; Score 502; DB 7; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MKLAALGLCVLSCSSAAFLVGSAPVQPVAALESAAEAGAGTLANPLGTINPLKLL 60
QY 61 LSSLGIPVNHLEIGSKVQVAVLGQVAVKALKALLGALTTFVG 104
DB 61 LSSLGIPVNHLEIGSKVQVAVLGQVAVKALKALLGALTTFVG 104

RESULT 32
ADA22531
ID ADA22531 standard; protein; 104 AA.
XX ADA22531;
AC ADA22531;
XX 20-NOV-2003 (first entry)
DE Human secreted/transmembrane polypeptide PRO1245.
KW human; tumour; cancer; colorectal cancer; gene therapy;
KW chondrocyte differentiation; VEGF inhibition;
KW vascular endothelial growth factor; Alzheimer's disease;
KW Parkinson's disease; atherosclerosis; cystic fibrosis;
KW multiple sclerosis; ovarian cancer; tissue typing.
XX Homo sapiens.
XX US2003040473-A1.
XX 27-FEB-2003.
XX 19-NOV-2001; 2001US-00989726.
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PR 02-JUL-1998; 98US-0091628P.  
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PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
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PR 30-JUL-1998; 98US-0094651P.  
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PR 11-AUG-1998; 98US-0096146P.  
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PR 05-JAN-1999; 98US-01000106.  
PR 08-MAR-1999; 98US-01005028.  
PR 12-MAR-1999; 98US-0123957P.  
PR 02-JUN-1999; 98US-0123952P.  
PR 23-JUN-1999; 98US-0140377P.  
PR 07-JUL-1999; 98US-0143048P.  
PR 20-JUL-1999; 98US-0144758P.  
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PR 28-JUL-1999; 98US-0146222P.

PR 17-AUG-1999; 99US-0149396P.  
PR 15-SEP-1999; 99US-0149396P.  
PR 15-SEP-1999; 99US-0149396P.  
PR 08-OCT-1999; 99US-0158663P.  
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PR 16-DEC-1999; 99US-0158663P.  
PR 20-DEC-1999; 99US-0158663P.  
PR 05-JAN-2000; 2000US-0000319.  
PR 06-JAN-2000; 2000US-0000376.  
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PR 24-FEB-2000; 2000US-0004914.  
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PR 23-AUG-2000; 2000US-0203522.  
  
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Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
  
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DB 1 MKLAALGICVALSCSSAAFLVGSAPVAPVAALESAAAGAGTLANPLGTLNPKLL 60  
  
QY 61 LSLGIPVNHLEIGSKQKVAELGPOAVGAVKALKALLGALTVP 104  
DB 61 LSLGIPVNHLEIGSKQKVAELGPOAVGAVKALKALLGALTVP 104  
  
RESULT 34  
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ID ADA06697 standard; protein; 104 AA.  
XX AC ADA06697;  
XX DT 29-JAN-2004 (revised)  
XX DT 06-NOV-2003 (first entry)  
XX DE Human secreted/transmembrane PRO polypeptide #127.  
XX KW human; tissue typing; cardiac insufficiency disorder; angiogenesis;  
XX KW wound healing; tumour; immune response; retinal disorder; retinal injury;  
XX KW sight loss; age-related macular degeneration; AMD; kidney disorder;  
XX KW mesangial cell function; Berger disease; nephropathy; dermatitis;  
XX KW herpeticiform; Crchn's disease; sports injury; arthritis.  
XX OS Homo sapiens.  
XX PN US2003049638-A1.  
XX PD 13-MAR-2003.  
XX PF 16-NOV-2001; 2001US-009991157.  
XX PR 16-JUN-1997; 97US-0049787P.  
XX PR 17-OCT-1997; 97US-0062250P.  
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PR	23-JUN-1998;	98US-0090349P.	PR	26-AUG-1998;	98US-0097955P.
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PR	24-JUN-1998;	98US-0090429P.	PR	26-AUG-1998;	98US-0097974P.
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PR	24-JUN-1998;	98US-0090445P.	PR	26-AUG-1998;	98US-0098014P.
PR	24-JUN-1998;	98US-0090472P.	PR	31-AUG-1998;	98US-0098525P.
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PR	17-SEP-1998;	98US-0100858P.
PR	17-SEP-1998;	98WO-US019437.
PR	07-OCT-1998;	98WO-US021141.
PR	01-DEC-1998;	98WO-US025108.
PR	22-DEC-1998;	98US-0113296P.
PR	05-JAN-1999;	98WO-US000106.
PR	08-MAR-1999;	98WO-US005028.
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PR	02-JUN-1999;	98WO-US012252.
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PR	07-JUL-1999;	98US-0143048P.
PR	20-JUL-1999;	98US-0144758P.
PR	26-JUL-1999;	98US-0145698P.
PR	28-JUL-1999;	98US-0146222P.
PR	17-AUG-1999;	98US-0149396P.
PR	15-SEP-1999;	98WO-US021090.
PR	15-SEP-1999;	98WO-US021547.
PR	08-OCT-1999;	99US-0158663P.
PR	30-NOV-1999;	99WO-US028313.
PR	01-DEC-1999;	99WO-US028301.
PR	01-DEC-1999;	99WO-US028634.
PR	16-DEC-1999;	99WO-US030095.
PR	20-DEC-1999;	99WO-US030911.
PR	05-JAN-2000;	2000WO-US000219.
PR	06-JAN-2000;	2000WO-US000376.
PR	11-FEB-2000;	2000WO-US003565.
PR	18-FEB-2000;	2000WO-US004341.
PR	22-FEB-2000;	2000WO-US004414.
PR	24-FEB-2000;	2000WO-US004914.
PR	24-FEB-2000;	2000WO-US005004.
PR	02-MAR-2000;	2000WO-US005841.
PR	10-MAR-2000;	2000WO-US006319.
PR	15-MAR-2000;	2000WO-US006884.
PR	20-MAR-2000;	2000WO-US007377.
PR	30-MAR-2000;	2000WO-US008439.
PR	15-MAY-2000;	2000WO-US013358.
PR	17-MAY-2000;	2000WO-US013705.
PR	22-MAY-2000;	2000WO-US014042.
PR	30-MAY-2000;	2000WO-US014941.
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PR	23-JUN-2000;	2000US-0213637P.
Query Match 100.0%; Score 502; DB 7; Length 104;		
Best Local Similarity 100.0%; Pred. No. 1.4e-48;		
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DB	1	MKLAALIGLCVALSCSSAAAFVGSAPVQPVAALESAAEACGTLANPLGTINPKLL 60
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DB	61	LSSLGIPVNHLEIGSKVVAELGPQAVGAVKALKALLGALTIVFG 104
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XX	ADB96416	standard; protein; 104 AA.
AC	ADB96416;	
XX	ADB96416;	
DT	04-DEC-2003	(first entry)
XX	Human PRO polypeptide #127.	
DE	Human PRO; pancreatic beta-cell precursor cell; pancreatic beta-cell;	
KW	insulin deficiency; diabetes mellitus; haemoglobin-associated disorder;	
KW	thalassaemia; endothelial cell growth; cancer; cystic renal dysplasia;	
KW	polycystic kidney disease; renal tumour; antidiabetic; antianemic;	
KW	cytostatic; cardiac; vulnery; antiinflammatory; anorectic.	
XX	Homo sapiens.	
OS	US2003054403-A1.	
PN	20-MAR-2003.	
XX	15-NOV-2001; 2001US-00997559.	
PF	16-JUN-1997;	97US-0049787P.
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PR	12-NOV-1997;	97US-0065186P.
PR	13-NOV-1997;	97US-0065311P.
PR	24-NOV-1997;	97US-0066770P.
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PR	20-MAR-1998;	98US-0078910P.
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PR	07-MAY-1998;	98US-0084600P.
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PR 09-JUL-1998; 98US-0092182P.  
PR 10-JUL-1998; 98US-0092472P.  
PR 20-JUL-1998; 98US-0093339P.  
PR 30-JUL-1998; 98US-0094651P.  
PR 04-AUG-1998; 98US-0095282P.  
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PR 23-JUN-1999; 98US-0141037P.  
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PR 15-SEP-1999; 98US-015021547.  
PR 08-OCT-1999; 98US-0158663P.  
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 PR 24-FEB-2000; 2000WO-US004914.  
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 PR 10-MAR-2000; 2000WO-US005841.  
 PR 15-MAR-2000; 2000WO-US006319.  
 PR 20-MAR-2000; 2000WO-US006884.  
 PR 30-MAR-2000; 2000WO-US007377.  
 PR 15-MAY-2000; 2000WO-US013358.  
 PR 17-MAY-2000; 2000WO-US013705.  
 PR 22-MAY-2000; 2000WO-US014042.  
 PR 30-MAY-2000; 2000WO-US014941.  
 PR 02-JUN-2000; 2000WO-US015264.  
 PR 23-JUN-2000; 2000US-0213637P.  
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 PR 23-AUG-2000; 2000WO-US023522.  
 Query Match 100.0%; Score 502; DB 7; Length 104;  
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 DB 1 MKLAALLGLCVALSAAFLVGSAPVAPVAALESAAEAGCTLANPLGTINPLKLL 60  
 OY 61 LSSLGIPVNHLEIGSKQVAFELGPQAVGAVKALKALLGALTTFVG 104  
 DB 61 LSSLGIPVNHLEIGSKQVAFELGPQAVGAVKALKALLGALTTFVG 104  
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 ADC55252  
 ID ADC55252 standard; protein; 104 AA.  
 XX AC ADC55252;  
 XX DT 18-DEC-2003 (first entry)  
 XX DE Human PRO polypeptide #127.  
 XX KW Human; PRO; pancreatic beta-cell precursor cell; pancreatic beta-cell;  
 KW insulin deficiency; diabetes mellitus; haemoglobin-associated disorder;  
 KW thalassaemia; endothelial cell growth; cancer; cystic renal dysplasia;  
 KW polycystic kidney disease; renal tumour; antidiabetic; antianemic;  
 KW cytostatic; cardiant; vulnery; antiinflammatory; anorectic.  
 XX OS Homo sapiens.  
 XX PN US2003045463-A1.  
 XX PD 06-MAR-2003.  
 XX PF 16-NOV-2001; 2001US-00990437.  
 XX PR 16-JUN-1997; 97US-0049787P.  
 PR 17-OCT-1997; 97US-0062250P.  
 PR 05-NOV-1997; 97WO-US020069.  
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 PR 13-NOV-1997; 97US-0085311P.  
 PR 24-NOV-1997; 97US-0086770P.  
 PR 25-FEB-1998; 98US-0075945P.  
 PR 20-MAR-1998; 98US-0078910P.  
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 PR 07-MAY-1998; 98US-0084600P.  
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 09-JUL-1998; 98US-0092182P.  
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 PR 20-JUL-1998; 98US-0093339P.  
 PR 30-JUL-1998; 98US-0094651P.  
 PR 04-AUG-1998; 98US-0095282P.  
 PR 08-AUG-1998; 98US-0095285P.  
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 PR 04-AUG-1998; 98US-0095318P.  
 PR 04-AUG-1998; 98US-0095321P.  
 PR 10-AUG-1998; 98US-0095325P.  
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 PR 11-AUG-1998; 98US-0096143P.  
 PR 11-AUG-1998; 98US-0096146P.  
 PR 12-AUG-1998; 98US-0096329P.  
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PR 07-OCT-1998; 98WO-US021141.  
PR 01-DEC-1998; 98WO-US025108.  
PR 22-DEC-1998; 98US-0113296P.  
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PR 08-MAR-1999; 98WO-US005028.  
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PR 02-JUN-1999; 99WO-US012252.  
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PR 07-JUL-1999; 99US-0143048P.  
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PR 17-AUG-1999; 99US-0149396P.  
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PR 11-FEB-2000; 2000WO-US003565.  
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KW	vascular endothelial growth factor; VEGF-stimulated proliferation;	
KW	endothelial cell; T-lymphocyte proliferation; retinal neuron;	
KW	c-fos induction; adipocyte cell; chondrocyte differentiation;	
KW	pneumatic beta-cell precursor differentiation; gene therapy; tumour	
KW	cancer; human; colon cancer; lung cancer; breast cancer;	
KW	rod photoreceptor cell.	
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PN	US2003049681-A1.	
PD	13-MAR-2003.	
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PR 24-FEB-2000; 2000WO-US005004.
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Best Local Similarity 100.0%; Pred. No. 1.4e-48;
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XX AC ADCS6541;
XX DT 18-DEC-2003 (first entry)
XX DE Human PRO polypeptide #127.
XX KW Human; PRO; pancreatic beta-cell precursor cell; pancreatic beta-cell;
insulin deficiency; diabetes mellitus; haemoglobin-associated disorder;
thalassaemia; endothelial cell growth; cancer; cystic renal dysplasia;
polycystic kidney disease; renal tumour; antidiabetic; antianaemic;
cytostatic; cardiac; vulnery; antinflammatory; anorectic.
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XX PN US2003064375-A1.
XX PD 03-APR-2003.
XX PF 15-NOV-2001; 2001US-00997857.
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PR	22-JUN-1998;	98US-0090254P.
PR	23-JUN-1998;	98US-0090349P.
PR	23-JUN-1998;	98US-0090355P.
PR	24-JUN-1998;	98US-0090429P.
PR	24-JUN-1998;	98US-0090431P.
PR	24-JUN-1998;	98US-0090435P.
PR	24-JUN-1998;	98US-0090444P.
PR	24-JUN-1998;	98US-0090472P.
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PR	24-JUN-1998;	98US-0090540P.
PR	24-JUN-1998;	98US-0090542P.
PR	24-JUN-1998;	98US-0090557P.
PR	25-JUN-1998;	98US-0090576P.
PR	25-JUN-1998;	98US-0090678P.
PR	25-JUN-1998;	98US-0090690P.
PR	25-JUN-1998;	98US-0090694P.
PR	25-JUN-1998;	98US-0090695P.
PR	25-JUN-1998;	98US-0090696P.
PR	26-JUN-1998;	98US-0090863P.
PR	01-JUL-1998;	98US-0091360P.
PR	01-JUL-1998;	98US-0091544P.
PR	02-JUL-1998;	98US-0091478P.
PR	02-JUL-1998;	98US-0091519P.
PR	02-JUL-1998;	98US-0091626P.
PR	02-JUL-1998;	98US-0091628P.
PR	02-JUL-1998;	98US-0091633P.
PR	02-JUL-1998;	98US-0091646P.
PR	02-JUL-1998;	98US-0091673P.
PR	07-JUL-1998;	98US-0091978P.
PR	07-JUL-1998;	98US-0091982P.
PR	09-JUL-1998;	98US-0092182P.
PR	10-JUL-1998;	98US-0092472P.
PR	20-JUL-1998;	98US-0093339P.
PR	30-JUL-1998;	98US-0094651P.
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PR	04-AUG-1998;	98US-0095285P.
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PR	04-AUG-1998;	98US-0095318P.
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PR	04-AUG-1998;	98US-0095325P.
PR	04-AUG-1998;	98US-0095326P.
PR	10-AUG-1998;	98US-0095329P.
PR	10-AUG-1998;	98US-0096012P.
PR	11-AUG-1998;	98US-0096143P.
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PR	18-AUG-1998;	98US-0096949P.
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PR	18-AUG-1998;	98US-0096953P.
PR	18-AUG-1998;	98US-0096960P.
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PR	19-AUG-1998;	98US-0097141P.
PR	20-AUG-1998;	98US-0097218P.
PR	26-AUG-1998;	98US-0097661P.
PR	26-AUG-1998;	98US-0097952P.
PR	26-AUG-1998;	98US-0097954P.
PR	26-AUG-1998;	98US-0097955

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PR 15-MAY-2000; 2000WO-US013358.
PR 17-MAY-2000; 2000WO-US013705.
PR 22-MAY-2000; 2000WO-US014042.
PR 30-MAY-2000; 2000WO-US014941.
PR 02-JUN-2000; 2000WO-US015264.
PR 23-JUN-2000; 2000US-0213637P.
PR 28-JUL-2000; 2000WO-US020710.
PR 11-AUG-2000; 2000WO-US022031.
PR 23-AUG-2000; 2000WO-US023522.

Query Match      100.0%; Score 502; DB 7; Length 104;
Best Local Similarity 100.0%; Pred. No. 1.4e-48;
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVALSCTSSAAAFVLGSAKPVQPVAALESAAEAGAGTIANPLGTINPLKLL 60
Db 1 MKLAALLGLCVALSCTSSAAAFVLGSAKPVQPVAALESAAEAGAGTIANPLGTINPLKLL 60

QY 61 LSSLGIPVNHLEGSQKCVAEELGPQAVGAVKALKALLGALTVEG 104
Db 61 LSSLGIPVNHLEGSQKCVAEELGPQAVGAVKALKALLGALTVEG 104
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Search completed: April 5, 2004, 14:34:07  
Job time : 58 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: April 5, 2004, 14:11:13 ; Search time 17 seconds  
(without alignments)  
318.547 Million cell updates/sec

Title: US-09-997-428-408  
Perfect score: 502  
Sequence: 1 MKLAALLGLCVSLSSGAAA.....QAVGAVKALKALGALTTFVG 104

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	437	99.0	104	UGR2_HUMAN	Q96qr1 homo sapien
2	250	49.8	104	UGR2_MOUSE	Q920d7 mus musculus
3	160	31.9	93	UGR1_HUMAN	Q96p11 homo sapien
4	135	26.9	139	UGR1_MOUSE	Q920h1 mus musculus
5	83	16.5	1327	TNK1_HUMAN	Q95271 homo sapien
6	77	15.3	335	TRD2_STRCO	Q924w3 streptomycete
7	76	15.1	732	COPA_HELPF	Q32619 helicobacte
8	75	14.9	362	MDC1_HUMAN	Q9h1k6 homo sapien
9	75	14.9	362	MDC1_MOUSE	Q9ere8 mus musculus
10	74	14.7	779	SNL1_MOUSE	Q60670 mus musculus
11	73.5	14.6	626	DXS_WIGBR	Q8d357 wiggleswort
12	73.5	14.6	776	SNL1_RAT	Q9rlu5 rattus norv
13	73.5	14.6	882	SYA_THETH	P4941 thermus the
14	72	14.3	397	SUCC_AGRIS	Q8uc60 agrobacteri
15	71	14.1	428	FXB2_MOUSE	Q64733 mus musculus
16	71	14.1	480	DNAA_RHIME	P35890 rhizobium m
17	69	13.7	124	RL7_RALSO	Q8xuz7 ralstonia s
18	68.5	13.6	377	PROB_BIFLO	Q8x4t9 bifidobacte
19	68	13.5	334	FEPP_ECOLI	P31876 escherichia
20	68	13.3	569	SILF_MOUSE	Q920g3 mus musculus
21	67.5	13.4	2035	I233_HUMAN	Q92508 homo sapien
22	67	13.3	351	GCP_MYCLE	P37969 mycobacteri
23	67	13.3	464	FUNC_PSESM	Q8B5v0 pseudomonas
24	66.5	13.2	341	TAZR_RAT	P34978 rattus norv
25	66.5	13.2	465	FXD1_HUMAN	Q16676 homo sapien
26	66	13.1	118	NLTD_BRAOL	Q43304 brassica ol
27	66	13.1	121	MP70_MYCKA	Q49614 mycobacteri
28	66	13.1	239	CLRC_IDEDE	P60000 ideonella d
29	66	13.1	527	FTB_MOUSE	P17225 mus musculus
30	66	13.1	540	LEVI_PROMM	Q7tuv5 prochloroco
31	66	13.1	585	NUP1_RAT	P70581 rattus norv
32	65.5	13.0	257	EUTC_RHOER	Q59782 rhodococcus
33	65.5	13.0	336	COBT_RHILO	Q98kn9 rhizobium l

RESULT 1

34	65.5	13.0	491	Y084_MYCTU	1	Y084_MYCTU
35	65	12.9	344	TRD2_RALSO	1	TRD2_RALSO
36	65	12.9	399	YM96_SYNEL	1	YM96_SYNEL
37	65	12.9	462	A2AC_HUMAN	1	A2AC_HUMAN
38	65	12.9	693	RECQ_ECOLI	1	RECQ_ECOLI
39	65	12.9	4377	ANK3_HUMAN	1	ANK3_HUMAN
40	64.5	12.8	184	CYCM_BRAJA	1	CYCM_BRAJA
41	64.5	12.8	320	E678_METJA	1	E678_METJA
42	64.5	12.8	750	ELS_CHICK	1	ELS_CHICK
43	64.5	12.8	905	NUOG_PSEAE	1	NUOG_PSEAE
44	64.5	12.8	1023	RT11_ACIFL	1	RT11_ACIFL
45	64.5	12.8	1023	RT12_ACIFL	1	RT12_ACIFL
46	64.5	12.8	1159	RPOC_PORCN	1	RPOC_PORCN
47	64.5	12.8	1608	HLYA_SERMA	1	HLYA_SERMA
48	64.5	12.8	2541	TLN1_HUMAN	1	TLN1_HUMAN
49	64	12.7	246	HIS4_METMA	1	HIS4_METMA
50	64	12.7	327	THI4_ASPOR	1	THI4_ASPOR
51	64	12.7	426	Y200_ANASP	1	Y200_ANASP
52	64	12.7	487	DNAA_AGRIS	1	DNAA_AGRIS
53	64	12.7	655	YAGF_ECOLI	1	YAGF_ECOLI
54	64	12.7	693	RECQ_ECO57	1	RECQ_ECO57
55	63.5	12.6	82	C551_PSEME	1	C551_PSEME
56	63.5	12.6	130	F14A_HUMAN	1	F14A_HUMAN
57	63.5	12.6	130	RL7_MYCLE	1	RL7_MYCLE
58	63.5	12.6	230	FLGH_XANCP	1	FLGH_XANCP
59	63.5	12.6	345	TRPD_AERPE	1	TRPD_AERPE
60	63.5	12.6	394	YGAY_ECO57	1	YGAY_ECO57
61	63.5	12.6	394	YGAY_ECOLI	1	YGAY_ECOLI
62	63.5	12.6	397	Y435_PROMA	1	Y435_PROMA
63	63.5	12.6	407	AROC_MYCLE	1	AROC_MYCLE
64	63.5	12.6	432	YF10_MYCTU	1	YF10_MYCTU
65	63.5	12.6	541	Y4MM_RHISN	1	Y4MM_RHISN
66	63.5	12.6	548	MEBA_PSEFL	1	MEBA_PSEFL
67	63.5	12.6	1048	P100_HCWVA	1	P100_HCWVA
68	63	12.5	434	YU18_MYCTU	1	YU18_MYCTU
69	63	12.5	435	YU21_MYCTU	1	YU21_MYCTU
70	63	12.5	517	6PGD_CANAL	1	6PGD_CANAL
71	63	12.5	932	PMS1_HUMAN	1	PMS1_HUMAN
72	63	12.5	1062	NAL2_HUMAN	1	NAL2_HUMAN
73	62.5	12.5	267	THIG_DEIRA	1	THIG_DEIRA
74	62.5	12.5	361	COBT_MYCTU	1	COBT_MYCTU
75	62.5	12.5	511	NADB_CAUCR	1	NADB_CAUCR
76	62.5	12.5	560	EFS_MOUSE	1	EFS_MOUSE
77	62.5	12.5	760	CO2_MOUSE	1	CO2_MOUSE
78	62	12.4	128	RL7_CORGL	1	RL7_CORGL
79	62	12.4	199	IL11_RAT	1	IL11_RAT
80	62	12.4	242	HIS4_HALN1	1	HIS4_HALN1
81	62	12.4	257	MOAB_KLEAE	1	MOAB_KLEAE
82	62	12.4	299	G3P_DICDI	1	G3P_DICDI
83	62	12.4	382	YN28_MYCTU	1	YN28_MYCTU
84	62	12.4	388	CHSD_PHANI	1	CHSD_PHANI
85	62	12.4	407	PCAB_PSEPU	1	PCAB_PSEPU
86	62	12.4	446	MURF_STRTO	1	MURF_STRTO
87	62	12.4	620	SNP_COTIA	1	SNP_COTIA
88	62	12.4	660	REP2_HUMAN	1	REP2_HUMAN
89	62	12.4	668	TKT_XANFL	1	TKT_XANFL
90	62	12.4	775	YTX1_XENLA	1	YTX1_XENLA
91	62	12.4	829	E74A_DROME	1	E74A_DROME
92	62	12.4	883	E74B_DROME	1	E74B_DROME
93	62	12.4	954	GCSP_AGRIS	1	GCSP_AGRIS
94	61.5	12.3	124	RL7_BRUME	1	RL7_BRUME
95	61.5	12.3	217	RNH2_AGRIS	1	RNH2_AGRIS
96	61.5	12.3	306	DDL_HAEIN	1	DDL_HAEIN
97	61.5	12.3	318	KIPF_XANCP	1	KIPF_XANCP
98	61.5	12.3	344	NAGK_HUMAN	1	NAGK_HUMAN
99	61.5	12.3	355	TRPD_AZOB	1	TRPD_AZOB
100	61.5	12.3	367	NK51_HUMAN	1	NK51_HUMAN

ALIGNMENTS

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UGR2_HUMAN
ID   UGR2_HUMAN          STANDARD;          PRT;   104 AA.
AC   Q96RL1; O96PL0;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in
DE   normal-1) (Secretoglobin family 3A member 1).
GN   SCGB3A1 OR UGRP2 OR HIN1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21396515; PubMed=11481438;
RA   Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P.,
RA   Kaelin C.M., Rhei E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z.,
RA   Belina D., Razumovic J., Polyak K.;
RT   "HIN-1, a putative cytokine highly expressed in normal but not
RT   cancerous mammary epithelial cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539178; PubMed=11682631;
RA   Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
RA   Kimura S.;
RT   "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is
RT   a novel lung-enriched downstream target gene for the 7/EBP/NKX2.1
RT   homeodomain transcription factor.";
RL   Mol. Endocrinol. 15:2021-2036(2001).
CC   -!- FUNCTION: Potential growth inhibitory cytokine.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- TISSUE SPECIFICITY: Highly expressed in breast tissues. Absent in
CC   breast cancer cell lines.
CC   -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; AY040564; AAK82942.1; .
DR   EMBL; AF313458; AAL26217.1; .
DR   Genbank; HGNC:18384; SCGB3A1.
DR   MIM; 606500; .
DR   GO; GO:0005576; C:extracellular; NAS.
DR   GO; GO:0005125; F:cytokine activity; NAS.
DR   GO; GO:0030308; P:negative regulation of cell growth; NAS.
DR   GO; GO:0042127; P:regulation of cell proliferation; NAS.
KW   Cytokine; Signal.
FT   SIGNAL          1    20    POTENTIAL.
FT   CHAIN          19    104    R -> A (IN REF. 2).
FT   CONFLICT      19    19      R -> A (IN REF. 2).
SQ   SEQUENCE      104 AA; 10185 MW; 1083873C8FAE8015 CRC64;

Query Match          99.0%; Score 497; DB 1; Length 104;
Best Local Similarity 99.0%; Pred. No. 7.2e-38;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy   1 MKLAALGLCVALSCSAAFLVGS AKPVAQPVAALSAEAGAGTLANPLGTLPKLL 60
Db   1 MKLAALGLCVALSCSAAFLVGS AKPVAQPVAALSAEAGAGTLANPLGTLPKLL 60

Qy   61 LSSLGIPVNHIEGSKQVAGLGPQAVGAVKALKALIGALTIVFG 104
Db   61 LSSLGIPVNHIEGSKQVAGLGPQAVGAVKALKALIGALTIVFG 104

RESULT 2

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UGR2_MOUSE
ID   UGR2_MOUSE          STANDARD;          PRT;   104 AA.
AC   Q920D7;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in
DE   normal-1) (Secretoglobin family 3A member 1).
GN   SCGB3A1 OR UGRP2 OR HIN1.
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21396515; PubMed=11481438;
RA   Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P.,
RA   Kaelin C.M., Rhei E., Bosenberg M., Schnitt S., Marks J.R., Pagon Z.,
RA   Belina D., Razumovic J., Polyak K.;
RT   "HIN-1, a putative cytokine highly expressed in normal but not
RT   cancerous mammary epithelial cells.";
RL   Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=21539178; PubMed=11682631;
RA   Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
RA   Kimura S.;
RT   "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is
RT   a novel lung-enriched downstream target gene for the 7/EBP/NKX2.1
RT   homeodomain transcription factor.";
RL   Mol. Endocrinol. 15:2021-2036(2001).
CC   -!- FUNCTION: Potential growth inhibitory cytokine.
CC   -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC   -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
DR   EMBL; AF313456; AAL26216.1; .
DR   MGD; MGI:1915912; SCGB3A1.
KW   Cytokine; Signal.
FT   SIGNAL          1    21    POTENTIAL.
FT   CHAIN          22    104    UTEROGLOBIN-RELATED PROTEIN 2.
SQ   SEQUENCE      104 AA; 10591 MW; D62F0E601FE57A6D CRC64;

Query Match          49.8%; Score 250; DB 1; Length 104;
Best Local Similarity 57.0%; Pred. No. 8.2e-16;
Matches 61; Conservative 14; Mismatches 26; Indels 6; Gaps 4;

Qy   1 MKL-AALLGLCVALSCSAAFLVGS AKPVAQPVAALSAEAGAGTLAN-PLGTLP 57
Db   1 MKLTTFLVLCVALLSDSGVAFPMDSLAKPAVEPVAALAPAAEAVAGVPSPLSHLAIL 60

Qy   58 KLLLSLGIPIVNHIEGSKQVAGLGPQAVGAVKALKALIGALTIVFG 104
Db   61 RFLIASMGIPLDPLIEGRKRCVTELGPEAVGAV---KSLLGVLTMFG 104

RESULT 3
UGR1_HUMAN
ID   UGR1_HUMAN          STANDARD;          PRT;   93 AA.
AC   Q96PL1;
DT   28-FEB-2003 (Rel. 41, Created)
DT   28-FEB-2003 (Rel. 41, Last sequence update)
DT   10-OCT-2003 (Rel. 42, Last annotation update)
DE   Uteroglobin-related protein 1 precursor (Secretoglobin family 3A
DE   member 2).
GN   SCGB3A2 OR UGRP1.

```

ID	UGRI_MOUSE
ID	UGRI_MOUSE STANDARD; PRT; 139 AA.
Q920H1	Q920H2; Q920H3;
AC	28-FEB-2003 (Rel. 41, Created)
DT	28-FEB-2003 (Rel. 41, Last sequence update)
DD	28-FEB-2003 (Rel. 41, Last annotation update)
DE	Uterogloblin-related protein 1 precursor (Secretogloblin family 3A member 2)
DN	SCGB3A2 OR UGRP1.
GN	Mus musculus (Mouse).
OS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OCC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI	TaxID=10090;
ON	[1]
RX	SEQUENCE FROM N.A. (ISOFORMS A; B AND C).
RP	TISSUE=Lung;
RC	MEDLINE=215361978; PubMed=1168231;
RA	Nimai T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C., Kimura S.;
RT	"UGRP1, a uterogloblin/clara cell secretory protein-related protein, is a novel lung-enriched downstream target gene for the T/BHP/NKX2.1 homeodomain transcription factor.";
RL	Mol. Endocrinol. 15:2021-2036(2001).
CC	- - SUBUNIT: Homodimer.
CC	- - SUBCELLULAR LOCATION: Secreted.
CC	- - ALTERNATIVE PRODUCTS:
CC	Event=Alternative splicing; Named isoforms=3;
CC	Name=C;
CC	IsoId=Q920H1-1; Sequence=Displayed;
CC	Name=A;
CC	IsoId=Q920H1-2; Sequence=VSP_006727, VSP_006728;
CC	Name=B;
CC	IsoId=Q920H1-3; Sequence=VSP_006726;
CC	- - TISSUE SPECIFICITY: Highly expressed in lung.
CC	- - SIMILARITY: Belongs to the uterogloblin family. UGRP subfamily.
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
EMBL	AF274959; AAL25708.1; -
EMBL	AF274960; AAL25709.1; -
EMBL	AF274961; AAL25710.1; -
MGI	GMI:2153470; Scgb3a2.
GO	GO:0005576; C:extracellular; IDA.
GO	GO:0005515; F:protein binding; IPI.
InterPro	IPR006038; Uterogloblin_supf.
Pfam	PF01099; Uterogloblin; 1.
KW	Signal; Alternative splicing.
SIGNAL	1 21 POTENTIAL.
FT CHAIN	22 139
FT FT	VARSPLIC 107 139
FT FT	UTEROGLOBLIN-RELATED PROTEIN 1.
FT FT	VSVLFLPMICAYPRDSKKQTAFIERVEQSKL -> EALS
FT FT	HLV (in isoform B).
FT FT	/FTID=VSP_006726.
FT FT	VARSPLIC 85 91 VIIICY -> EALSGLV (in isoform A).
FT FT	/FTID=VSP_006727.
FT FT	VARSPLIC 92 139 Missing (in isoform A).
FT FT	/FTID=VSP_006728.
FT FT	SEQUENCE 139 AA; 15431 MW; 8A2F803B4E85E4 CRC64;
Query Match	26.9%; Score 135; DB 1; Length 139;
Best Local Similarity	35.1%; Pred. No. 28-05;
Matches	34; Conservative 17; Mismatches 36; Indels 10; Gaps 1;
QY	1 MKIAALLGLCVASAAFLVGSAKPVAQPVAALSAAGAGCTLANPLGTLP.KLL 60
Dd	1 MKIWSIFLLVTIGCYSATLLINPLPVDVKLPV-----PLDIIPSDFPLKML 50
QY	61 LSSLGIPVNHLIEGSKVCVAELGPQAVGAVKALKALL 97

61 LSSLGIPVNHLEGSQKCV AELGPQAVGAVKALL 97

```

Db 51 LKTLGTSVEHLVTGLKCKVDLGPSEASAVKLLVII 87
RESULT 5
TNK1 HUMAN
ID TNK1 HUMAN STANDARD; PRT; 1327 AA.
AC C95271; C95272;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Tankyrase 1 (SC 2.4.2.30) (TANK1) (Tankyrase I) (TNKS-1) (TRF1-
DE interacting ankyrin-related ADP-ribose polymerase).
GN TNKS OR TNKS1 OR TINI OR TINF1 OR PARPL.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OC NCBI_Taxid=9606;
RN [1]
RN [2]
RN [3]
RP MEDLINE=99454782; PubMed=10523501;
RX Smith S., de Lange T.;
RT "Cell cycle dependent localization of the telomeric PAPP, tankyrase,
RT to nuclear pore complexes and centrosomes.";
RL J. Cell Sci. 112:3649-3656 (1999).
RN [3]
RN [3]
RP SUBCELLULAR LOCATION.
RX MEDLINE=99454782; PubMed=10523501;
RX Smith S., de Lange T.;
RT "Cell cycle dependent localization of the telomeric PAPP, tankyrase,
RT to nuclear pore complexes and centrosomes.";
RL J. Cell Sci. 112:3649-3656 (1999).
RN [3]
RN [3]
RP FUNCTION, AND PHOSPHORYLATION.
RX MEDLINE=20556282; PubMed=10988299;
RX Chi N.-W., Lodish H.F.;
RT "Tankyrase is a Golgi-associated mitogen-activated protein kinase
RT substrate that interacts with IRAP in GLUT4 vesicles.";
RL J. Biol. Chem. 275:38437-38444 (2000).
RN [4]
RN [4]
RP FUNCTION, AND MUTAGENESIS OF HIS-1184 AND GLU-1291.
RX Cook B.D., Dynek J.N., Chang W., Shostak G., Smith S.;
RT "Role for the related poly(ADP-Ribose) polymerase tankyrase 1 and 2
RT at human telomeres.";
RL Mol. Cell. Biol. 22:332-342 (2002).
CC -!- FUNCTION: May regulate vesicle trafficking and modulate the
CC subcellular distribution of SLIC2A4/GLUT4-vesicles. Has PAPP
CC activity and can modify TRF1, and thereby contribute to the
CC regulation of telomere length.
CC -!- CATALYTIC ACTIVITY: NAD(+) + {ADP-D-ribose}[(N)-acceptor =
CC nicotinamide + {ADP-D-ribose}[(N+1)-acceptor.
CC -!- SUBUNIT: Oligomerizes and associates with TNKS2. Interacts with
CC the cytoplasmic domain of INPEP/Otase in SLIC2A4/GLUT4-vesicles.
CC Binds to the N-terminus of telomeric TRF1 via the ANK repeats.
CC -!- SUBCELLULAR LOCATION: Cytoplasmic, associated with the Golgi and
CC with juxtanuclear SLIC2A4/GLUT4-vesicles. A minor proportion is
CC also found at nuclear pore complexes and around the pericentriolar
CC matrix of mitotic centrosomes. During interphase, a small fraction
CC of TNKS is found in the nucleus, associated with TRF1.
CC -!- ALTERNATIVE PRODUCTS:
CC Event=alternative splicing; Named isoforms=2;
CC Name=1;
CC IsoId=O95271-1; Sequence=Displayed;
CC Name=2;
CC IsoId=O95271-2; Sequence=VSP_004538, VSP_004539;
CC Note=No experimental confirmation available;
CC -!- TISSUE SPECIFICITY: Ubiquitous; highest levels in testis.
CC -!- PTM: Upon insulin-stimulation, phosphorylated on serine residues
CC by MAPK kinases.
CC -!- PTM: ADP-ribosylated (-auto).
CC -!- SIMILARITY: Belongs to the PAPP family.
CC -!- SIMILARITY: Contains 15 ANK repeats.

```

CC -!- SIMILARITY: Contains 1 sterile alpha motif (SAM) domain.

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CC EMBL; AF082556; AAC79841.1; -

CC EMBL; AF082557; AAC79842.1; -

CC EMBL; AF082558; AAC79843.1; -

CC EMBL; AF082559; AAC79844.1; -

CC HSP; Q00420; IAWC.78.

CC Genew; HGNC:11941; TNKS.

CC MM; G03303; -

CC GO; GO:000781; C:Chromosome, telomeric region; IDA.

CC GO; GO:0003950; F:NAD ADP-ribosyltransferase activity; IDA.

CC GO; GO:000515; F:protein binding; IPI.

CC GO; GO:0007004; P:telomerase-dependent telomere maintenance; NAS.

CC InterPro; IPR002110; ANK.

CC InterPro; IPR001660; SAM.

CC Pfam; PF00023; ank; 19.

CC Pfam; PF00036; SAM; 1.

CC PRINTS; PR01415; ANKYRIN.

CC SMART; SM00248; ANK; 17.

CC SMART; SM00454; SAM; 1.

CC PROSITE; PS00888; ANK REPEAT; 15.

CC PROSITE; PS0297; ANK REP REGION; 1.

CC PROSITE; PS0105; SAM DOMAIN; 1.

CC Transferase; Glycosyltransferase; NAD; Golgi stack; Telomere;

CC Nuclear protein; Repeat; ANK repeat; ADP-ribosylation;

CC Phosphorylation; Alternative splicing.

FT REPEAT 215 247 ANK 1.

FT REPEAT 248 280 ANK 2.

FT REPEAT 281 313 ANK 3.

FT REPEAT 368 400 ANK 4.

FT REPEAT 401 433 ANK 5.

FT REPEAT 434 466 ANK 6.

FT REPEAT 521 556 ANK 7.

FT REPEAT 557 589 ANK 8.

FT REPEAT 590 622 ANK 9.

FT REPEAT 683 715 ANK 10.

FT REPEAT 716 748 ANK 11.

FT REPEAT 749 781 ANK 12.

FT REPEAT 836 868 ANK 13.

FT REPEAT 869 901 ANK 14.

FT REPEAT 902 934 ANK 15.

FT DOMAIN 1030 1089 SAM.

FT DOMAIN 1176 1327 PAPP.

FT DOMAIN 9 14 POLY-HIS.

FT DOMAIN 27 34 POLY-PRO.

FT DOMAIN 128 134 POLY-SER.

FT DOMAIN 137 145 POLY-SER.

FT VARSPLIC 641 643 EST -> GHS (in isoform 2).

FT VARSPLIC 644 1327 /FTid=VSP\_004538.

FT VARSPLIC 644 1327 Missing (in isoform 2).

FT MUTAGEN 1184 1184 /FTid=VSP\_004539.

FT MUTAGEN 1291 1291 H->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1291.

FT MUTAGEN 1291 1291 E->A: LOSS OF ACTIVITY; WHEN ASSOCIATED WITH A-1184.

FT SEQUENCE 1327 AA; 142010 MW; E14DE985C710B957 CRC64;

Query Match 16.5%; Score 83; DB 1; Length 1327;

Best Local Similarity 30.5%; Pred.No. 6.5;

Matches 29; Conservative 13; Mismatches 43; Indels 10; Gaps 3;

QY 15 CSAAFLVGSAPVAPVQAQVALEGA-----EAGAGTLANPLGLNPLKLLSLGIPVN 69

DB 90 CATTCTICVAAPV-PAVSTSSAAGVAPNAGSGNNPSSSSSFTSSSSSSPSSPS 148

QY 70 HLIQSQ----KCVAGLPGQAVGAVKALLGAL 100  
Db 149 SLAESPERAGVSSTAPLPGGAAGTGTGVPVSGAL 183

## RESULT 6

TRD2\_STRCO  
AC Q924W9; STANDARD; PRT; 335 AA.

DT 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Anthranilate phosphoribosyltransferase 2 (SC 2.4.2.18).  
GN TRPD2 OR SCO3212 OR SCER.OSC.  
OS Streptomyces coelicolor.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomycineae; Streptomycetaceae; Streptomyces.

OK NCBI\_TaxID=1902;

RN [1]\_TaxID=1902;

RP SEQUENCE FROM N.A.

RX STRAIN=A3(2) / M145;

RC MEDLINE=21996410; PubMed=12000953;

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kieser T., Larke I., Murphy L., Oliver K., O'Neil S.,

RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S., Taylor K.,

RA Seeger K., Saunders D., Sharp S., Squares R., Squares R., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J., Barrall B.G., Parkhill J.,

RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2)";

RL Nature 417:141-147(2002).

CC -!- CATALYTIC ACTIVITY: Anthranilate + phosphoribosyl-diphosphate =

CC N-5'-phosphoribosyl-anthranilate + diphosphate.

CC -!- PATHWAY: Tryptophan biosynthesis; second step.

CC -!- SIMILARITY: Belongs to the anthranilate phosphoribosyltransferase

CC family.

CC

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CC

CC EMBL; AL939115; CAB38583.1; -.

DR PIR; T36304; T36304.

DR HAMAP; MF\_00211; -; 1.

DR InterPro; IPR005940; Ant. phsopho trans.

DR InterPro; IPR000312; Glyco trans 3.

DR Pfam; PR02885; Glycos trans 3N; 1.

DR Pfam; PR00591; Glycos\_trans\_3; 1.

DR ProDom; PD001864; Glyco\_trans\_3; 1.

DR TIGRFAMs; TIGR01245; trp; 1.

DR Tryptophan biosynthesis; Transferase; Glycosyltransferase;

KW Complete proteome.

SQ SEQUENCE 335 AA; 34536 MW; 2706194E400B2F0D CRC64;

Query Match 15.3%; Score 77; DB 1; Length 335;

Best Local Similarity 34.5%; Pred. No. 6.5; Indels 12; Gaps 4;

Matches 30; Conservative 9; Mismatches 36;

QY 7 LGUCVALSCSSAAAFVLSGA-----KFAQPVVALESAA-----EAGATLANPLGTL-NP 56

Db 117 LGVRIDLGAEAAACLDRTGTFAPVFP--AFRHTAGPRRELGAFTVNLGLPLCNP 174

QY 57 LKLLLSLGIPIVNHLEQSKQCVAGLG 83

Db 175 SGARLRTLGVPSELVEPMTVEVLRLG 201

## RESULT 7

COPA\_HELPFE

ID COPA\_HELPFE

AC O32619;

DT 15-JUL-1998 (Rel. 36, Created)

DT 15-JUL-1998 (Rel. 36, Last sequence update)

DT 15-MAR-2004 (Rel. 43, Last annotation update)

DE Copper-transporting ATPase (SC 3.6.3.4).

GN COPA.

OS Helicobacter felis.

OC Bacteria; Proteobacteria; Epsilonproteobacteria; Campylobacteriales;

OC Helicobacteraceae; Helicobacter.

OK NCBI\_TaxID=214;

RN [1]\_TaxID=214;

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 49179;

RX MEDLINE=98101471; PubMed=9440521;

RA Bayle D., Waengler S., Weitzenecker T., Steinhilber W., Volz J.,

RA Przybylski M., Schaefer K.P., Sachs G., Melchers K.;

RT "Properties of the P-type ATPases encoded by the copA operons of

RT Helicobacter pylori and Helicobacter felis";

RL J. Bacteriol. 180:317-329(1998).

CC -!- FUNCTION: PROBABLY INVOLVED IN COPPER EXPORT.

CC -!- CATALYTIC ACTIVITY: ATP + H(2)O + Cu(2+) (in) = ADP + phosphate +

CC Cu(2+) (out).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- SIMILARITY: Belongs to the cation transport ATPases family (P-type

CC ATPases). Subfamily IB.

CC -!- SIMILARITY: Contains 1 HMA domain.

CC

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CC

CC EMBL; AJ001932; CA005104.1; -.

DR PIR; T47269; T47269.

DR InterPro; IPR006403; ATPase-IB1 Cu.

DR InterPro; IPR006416; ATPase-IB Hvy.

DR InterPro; IPR001757; ATPase\_EI-E2.

DR InterPro; IPR001756; Cu\_ATPase.

DR InterPro; IPR008250; EI-E2 ATPase\_reg.

DR InterPro; IPR006121; Heavy\_Me\_transpt.

DR InterPro; IPR005834; Hydrolase.

DR InterPro; IPR006191; Metal\_bind.

DR Pfam; PR00122; EI-E2 ATPase; 1.

DR Pfam; PR00702; HMA; 1.

DR PRINTS; PR00119; CATATPASE.

DR PRINTS; PR00943; CUATPASE.

DR TIGRFAMs; TIGR01511; ATPase-IB1 Cu; 1.

DR TIGRFAMs; TIGR01525; ATPase-IB Hvy; 1.

DR TIGRFAMs; TIGR01494; ATPase\_P-type; 3.

DR PROSITE; PS00354; ATPase\_EI-E2; 1.

DR PROSITE; PS01047; HMA\_1; 1.

DR PROSITE; PS00846; HMA\_2; 1.

KW Transport; Ion transport; Copper transport; Hydrolase; ATP-binding;

KW Metal-binding; Copper; Magnesium; Transmembrane; Phosphorylation.

FT DOMAIN 1 88

FT TRANSMEM 89 109

FT DOMAIN 110 122

FT TRANSMEM 123 142

FT DOMAIN 143 149

FT TRANSMEM 150 170

FT DOMAIN 171 187

FT TRANSMEM 188 208

FT DOMAIN 209 336

FT TRANSMEM 337 359

FT DOMAIN 360

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FT TRANSMEM 366 383 POTENTIAL.
FT DOMAIN 384 663 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 664 683 POTENTIAL.
FT DOMAIN 684 694 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 695 713 POTENTIAL.
FT DOMAIN 714 732 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 732 732 HNA.
FT MOD RES 421 421 PHOSPHORYLATION (BY SIMILARITY).
FT METAL 13 13 COPPER (POTENTIAL).
FT METAL 16 16 COPPER (POTENTIAL).
FT METAL 609 609 MAGNESIUM (BY SIMILARITY).
FT METAL 613 613 MAGNESIUM (BY SIMILARITY).
FT METAL 732 732 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 732 AA; 78853 MW; 7105107EA949EFD CRC64;

Query Match 15.1%; Score 76; DB 1; Length 732;
Best Local Similarity 26.3%; Pred. No. 16;
Matches 35; Conservative 17; Mismatches 39; Indels 42; Gaps 6;

Qy 6 LLGLCVALSCTSAAPFVGSAPKPAQVPAAL-----ESAAEAGAG----- 45
Db 447 LLLTCLASLEAQSHVIAKGVIAHAKEGIALQEVQVQAKPFGIKGVVGDQIIKAGNLE 506
Qy 46 --TIANPLGTNPKLLSS-----LGPV--NHLIEGSKCVABLGPOAVGA----- 89
Db 507 FFNLNPFGLTGLQVFGVGTQILGVVWLADSLKEGSKAISEL--KALGVKTTLLSGD 564
Qy 90 -----VKALKALLG 98
Db 565 NLENVRALATQLG 577

RESULT 8
MDC1_HUMAN
ID MDC1_HUMAN STANDARD; PRT; 362 AA.
AC Q9HIK6;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Mesoderm development candidate 1.
GN MESDC1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Retina;
RX MEDLINE=21145589; PubMed=11247670;
RA Wines M.E., Lee L., Katari M.S., Zhang L., DeRossi C., Shi Y.,
RA Perkins S., Feldman M., McCombie W.R., Holdener B.C.;
RA "Identification of mesoderm development (mesd) candidate genes by
RT comparative mapping and genome sequence analysis.";
RL Genomics 72:88-98(2001).
CC -!- SIMILARITY: SOME, TO TALIN.
CC
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CC
CC EMBL; AY007810; AAG41058.1; -
CC Genew; HGNC:13519; MESDC1.
SQ SEQUENCE 362 AA; 37758 MW; 37BF391D663B1D6E CRC64;

Query Match 14.9%; Score 75; DB 1; Length 362;
Best Local Similarity 35.4%; Pred. No. 11;
Matches 28; Conservative 6; Mismatches 33; Indels 12; Gaps 3;

Qy 3 LAALLGLCVALS-CSSAAAFVGSAPKPAQV-----VAALSAAGAGTTL-ANP 50

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```

Db 112 LVLEGLDVVSLTECSAAHYLAAVATPGAQPAQGLVDYRVYVTRCRHEVQGCVALRATP 171
Qy 51 LGTNPLKLLSSLGIPVN 69
Db 172 LADMTFOLLLEVSQGLSRN 190

RESULT 9
MDC1_MOUSE
ID MDC1_MOUSE STANDARD; PRT; 362 AA.
AC O9REB8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Mesoderm development candidate 1.
GN MESDC1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC STRAIN=129/SvJ;
RX MEDLINE=21145589; PubMed=11247670;
RA Wines M.E., Lee L., Katari M.S., Zhang L., DeRossi C., Shi Y.,
RA Perkins S., Feldman M., McCombie W.R., Holdener B.C.;
RA "Identification of mesoderm development (mesd) candidate genes by
RT comparative mapping and genome sequence analysis.";
RL Genomics 72:88-98(2001).
CC [2]
CC SEQUENCE FROM N.A.
RP MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.S., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McSwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Pahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smallos D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RA "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -!- TISSUE SPECIFICITY: Ubiquitous.
CC -!- SIMILARITY: SOME, TO TALIN.
CC
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CC
CC EMBL; AF311213; AAG33620.1; -
CC DR EMBL; BC018326; AAH18326.1; -
CC DR MGD; MGI:1891420; Mesdcl.
SQ SEQUENCE 362 AA; 37786 MW; EFE9BBFC09BB7CB5 CRC64;

Query Match 14.9%; Score 75; DB 1; Length 362;
Best Local Similarity 35.4%; Pred. No. 11;
Matches 28; Conservative 6; Mismatches 33; Indels 12; Gaps 3;

Qy 3 LAALLGLCVALS-CSSAAAFVGSAPKPAQV-----VAALSAAGAGTTL-ANP 50

```

```
Db 112 LEVELGVSVTECSAHAAAYLAATVATGQAQGLVDRVTRCRHEVVGCAVLRATP 171
QY 51 LGTINPLKLLLSGLGIPVN 69
Db 172 LADMTFQQLLEVSQGLSRN 190

RESULT 10
SNIL_MOUSE
ID SNIL_MOUSE STANDARD; PRT; 779 AA.
AC Q60670;
DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-MAR-2004 (Rel. 43, Last annotation update)
DE Probable serine/threonine protein kinase SNF1LK (EC 2.7.1.1.-) (HRT-20)
DE (Myocardial SNF1-like kinase).
GN SNF1LK OR MSK.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Musinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND REVISIONS TO 8; 16-18; 44-45; 316 AND 435.
RC TISSUE=Embryo;
RA Ruiz J.C.;
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 1-435 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Embryo;
RX MEDLINE=95200798; PubMed=7893599;
RA Ruiz J.C., Conlon F.L., Robertson E.J.;
RT "Identification of novel protein kinases expressed in the myocardium
of the developing mouse heart.";
RL Mech. Dev. 48:153-164(1994).
CC -!- TISSUE SPECIFICITY: Expressed in lung, skin, ovary, heart and
CC stomach. No expression in brain, liver or skeletal muscle.
CC -!- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -!- SIMILARITY: Contains 1 UBA domain.
CC
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CC
CC EMBL; U11494; AAA67926.2; -
CC HSSP; P24941; 1AQL.
CC MGD; MGI:104754; Snflk.
CC InterPro; IPR000719; Prot_kinase.
CC InterPro; IPR008271; Ser_thr_pkin_AS.
CC InterPro; IPR002290; Ser_thr_pkinase.
CC InterPro; IPR001245; Tyr_pkinase.
CC InterPro; IPR000449; UBA_domain.
CC Pfam; PF00669; pkinase; 1.
CC PRINTS; PR00109; TYRKINASE.
CC ProDom; PD000001; Prot_kinase; 1.
CC SMART; SM00220; S_TKc; 1.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
CC PROSITE; PS00111; PROTEIN_KINASE_DOM; 1.
CC PROSITE; PS00108; PROTEIN_KINASE_ST; 1.
CC PROSITE; PS00300; UBA; 1.
CC Transferrase; Serine/threonine-protein kinase; ATP-binding.
KW DOMAIN 27 278 PROTEIN KINASE.
FT DOMAIN 303 343 UBA.
FT NP_BIND 33 41 ATP (BY SIMILARITY).
FT BINDING 56 56 ATP (BY SIMILARITY).
FT ACT_SITE 149 149 BY SIMILARITY.
FT ACT_SITE 779 AA; 85027 MW; 7808131BC46D9C4E CRC64;
SQ SEQUENCE
```

```
Query Match 14.7%; Score 74; DB 1; Length 779;
Best Local Similarity 32.9%; Pred.No. 26;
Matches 26; Conservative 11; Mismatches 30; Indels 12; Gaps 3;

QY 10 CVALSCSSAAFLVGSAPVQAPVAALESAAEAGAGTLANP--LGTINPLKLLLSGLGIP 67
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 490 CIIVSSSATASPSGTSCLPFSASEGPAGLGG-LATPGLLTGTSPPVRLASPEL--- 545
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

QY 68 VNHLEGSOKVAVELGPOA 86
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|
Db 546 -----GQSATPVLQTA 558
|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|::|

RESULT 11
DXS_WIGBR
ID DXS_WIGBR STANDARD; PRT; 626 AA.
AC Q8D557;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE 1-deoxy-D-xylulose 5-phosphate synthase (EC 2.2.1.7) (1-
DE deoxyxylulose-5-phosphate synthase) (DXP synthase) (DXPS).
GN DXS OR WIGBR1440
OS Wigglesworthia glossinidia brevipalpis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Wigglesworthia.
OX NCBI_TaxID=36870;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22297718; PubMed=12219091;
RA Akman L., Yamashita A., Watanabe H., Oshima K., Shiba T., Hattori M.,
RA Aksoy S.;
RT "Genome sequence of the endocellular obligate symbiont of tsetse
RT flies, Wigglesworthia glossinidia.";
RL Nat. Genet. 32:402-407(2002).
CC -!- FUNCTION: Catalyzes the acyloin condensation reaction between C
CC atoms 2 and 3 of pyruvate and glyceraldehyde 3-phosphate to yield
CC 1-deoxy-D-xylulose-5-phosphate (DXP) (By similarity).
CC -!- CATALYTIC ACTIVITY: Pyruvate + D-glyceraldehyde 3-phosphate = 1-
CC deoxy-D-xylulose 5-phosphate + CO(2).
CC -!- COFACTOR: Binds 1 thiamine pyrophosphate per subunit (By
CC similarity).
CC -!- PATHWAY: Nonmevalonate terpenoid biosynthesis pathway; first step.
CC -!- PATHWAY: Biosynthetic pathway to thiamine and pyridoxol; first
CC step.
CC -!- SUBUNIT: Homodimer (By similarity).
CC -!- SIMILARITY: Belongs to the transketolase family. DXPS subfamily.
CC
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CC
CC EMBL; AB063521; BAC24290.1; -
CC HAMAP; MF_00315; -; 1.
CC InterPro; IPR005477; Dxs_synth.
CC InterPro; IPR009014; Transketolase_C_like.
CC InterPro; IPR005476; Transketolase_C.
CC InterPro; IPR005475; Transketolase_CR.
CC InterPro; IPR005474; Transketolase_N.
CC Pfam; PF02779; transket_pvr; 1.
CC Pfam; PF02780; transketolase_C; 1.
CC TIGRFAMs; TIGR00204; dxs; 1.
CC PROSITE; PS00801; TRANSKETOLASE_1; 1.
CC PROSITE; PS00802; TRANSKETOLASE_2; FALSE NEG.
KW Transferrase; Flavoprotein; Thiamine pyrophosphate;
KW Isoprene biosynthesis; Thiamine biosynthesis; Complete proteome.
SQ SEQUENCE 626 AA; 69851 MW; C77008D2D82ABE21 CRC64;

Query Match 14.6%; Score 73.5; DB 1; Length 626;
```

```
Best Local Similarity 30.0%; Pred. No. 24;
Matches 24; Conservative 14; Mismatches 41; Indels 1; Gaps 1;

QY 22 LVGSAKPVQAFVAALSAEAGAGTLANPLGTLNPKLLSLGIPVNHLEGSQKCV-A 80
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 546 LIRMAKTHKALITIEENVINGGSAVNEFIMYNKLLVPLNIGIPDNFVSHGSGTEVRS 605
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 81 ELGPOAVGAVKALKALIGAL 100
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 606 SLGDSIGIKKIKWLNFL 625
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 12
SN1L_RAT SN1L_RAT STANDARD; PRT; 776 AA.
AC Q9R1J5; Q9R081;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Probable serine/threonine protein kinase SNF1LK (EC 2.7.1.-) (Salt-
DE inducible protein kinase) (Protein kinase KID2).
GN SNF1LK OR SIK OR KID2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
SEQUENCE FROM N.A.
RP STRAIN=Sprague-Dawley; TISSUE=Adrenal gland;
RX MEDLINE=99303184; PubMed=10403390;
RA Wang Z., Takemori H., Halder S.K., Nonaka Y., Okamoto M.;
RT "Cloning of a novel kinase (SIK) of the SNF1/AMPK family from high
RT salt diet-treated rat adrenal.";
RL FEBS Lett. 453:135-139 (1999).
[2]
SEQUENCE FROM N.A.
RP Feldman J.D., Vician L., Crispino M., Hoe W., Baudry M.,
RA Herschman H.R.;
RT "The Kid2 gene encodes a protein kinase induced by depolarization in
RT brain.";
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: Belongs to the Ser/Thr family of protein kinases. SNF1
CC subfamily.
CC -1- SIMILARITY: Contains 1 UBA domain.
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CC or send an email to license@isb-sib.ch).
CC EMBL; AB020480; BAA92673.1; -
DR EMBL; AF106937; AAF14191.1; -
DR HSP; P24941; 1AQ1.
DR InterPro; IPR000719; Prot kinase.
DR InterPro; IPR008271; Ser Thr pkin AS.
DR InterPro; IPR002290; Ser-Chr pkinase.
DR InterPro; IPR000449; UBA_domain.
DR Pfam; PF00063; Pkinase; 1.
DR ProDom; PD000001; Prot kinase; 1.
DR SMART; SM00220; S_TKc; 1.
DR PROSITE; PS00107; PROTEIN KINASE ATP; 1.
DR PROSITE; PS00111; PROTEIN KINASE DOM; 1.
DR PROSITE; PS0108; PROTEIN_KINASE_St; 1.
DR PROSITE; PS0030; UBA; 1.
KW Transferase; Serine/threonine-protein kinase; ATP-binding.
FT DOMAIN 27 278 PROTEIN KINASE.
FT DOMAIN 303 343 UBA.
FT NP_BIND 33 41 ATP (BY SIMILARITY).
FT BINDING 56 56 ATP (BY SIMILARITY).
FT ACT_SITE 149 149 BY SIMILARITY.
```

```
FT CONFLICT 473 473 R -> K (IN REF. 2).
SQ SEQUENCE 776 AA; 84908 MW; 7BF745AF28F17E6E CRC64;

Query Match 14.6%; Score 73.5; DB 1; Length 776;
Best Local Similarity 33.7%; Pred. No. 28;
Matches 28; Conservative 11; Mismatches 31; Indels 13; Gaps 4;

QY 10 CVALSCSSAAFLVGSAPVQAFVAALSAEAGAGTLANP--LGTNLPKLLSLGIP 67
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 490 CTVVSSAAVSPSEGTSDSCLPFSASEGPAGLGG-LATPGLLTGSPVRLASPFLL--- 545
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 68 VNHLEGSQKCVAEIGPOA-VGA 89
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 546 -----GSQATPVLQSQAGLGA 562
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 13
SYA_THETH STANDARD; PRT; 882 AA.
ID P74941;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Alanyl-tRNA synthetase (EC 6.1.1.7) (Alanine--tRNA ligase) (ALARS).
GN ALAS
OS Thermus thermophilus.
OC Bacteria; Deinococcus-Thermus; Deinococci; Thermales; Thermaceae;
OX NCBI_TaxID=274;
RN [1]
SEQUENCE FROM N.A.
RC STRAIN=HB8 / ATCC 27634;
RX MEDLINE=97351141; PubMed=9207019;
RA Lechter A., Martin A., Zuleeg T., Limmer S., Kreutzer R.;
RT "A biologically active 53 kDa fragment of overproduced alanyl-tRNA
RT synthetase from Thermus thermophilus HB8 specifically interacts with
RT tRNA ala acceptor helix.";
RL Nucleic Acids Res. 25:2737-2744 (1997).
CC -1- CATALYTIC ACTIVITY: ATP + L-alanine + tRNA(Ala) = AMP +
CC diphosphate + L-alanyl-tRNA(Ala).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: Belongs to class-II aminoacyl-tRNA synthetase family.
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CC or send an email to license@isb-sib.ch).
CC EMBL; Y08363; CAA69650.1; -
DR HAMAP; MF 00036; -; 1.
DR InterPro; IPR003156; DHHA1.
DR InterPro; IPR002318; tRNA-synt_2c.
DR Pfam; PF006193; tRNA_synt_Ala.
DR Pfam; PF02272; DHHA1; 1.
DR Pfam; PF01411; tRNA-synt_2c; 1.
DR PRINTS; PR00980; TRNASYNTHALA.
DR TIGRFAMs; TIGR00344; alaS; 1.
DR PROSITE; PS50860; AA tRNA LIGASE II ALA; 1.
KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding.
SQ SEQUENCE 882 AA; 97454 MW; E60E3E34480CFC56 CRC64;

Query Match 14.6%; Score 73.5; DB 1; Length 882;
Best Local Similarity 32.6%; Pred. No. 32;
Matches 30; Conservative 12; Mismatches 47; Indels 3; Gaps 2;

QY 6 LLGLCVALSCSSAAFLVGSAPVQAFVAALSAEAGAGTLANPLGTLNPKLLSLG 65
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 681 LCGGCHVRFTGTGALIRSEAVSAGVRIE--AVTGEAIRFARGSLNRUKLAERLE 738
   : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

QY 66 IPVNHLEGSQKCVAEIGPOAVGAVKALKAL 97
```

KW Ligase; Tricarboxylic acid cycle; Complete proteome.  
SQ SEQUENCE 397 AA; 41899 MW; 223CIA3825764F9F CRC64;  
  
Query Match 14.3%; Score 72; DB 1; Length 397;  
Best Local Similarity 36.2%; Pred. No. 21;  
Matches 29; Conservative 8; Mismatches 31; Indels 12; Gaps 4;  
  
QY 18 AAAPLVGSAXFVAQPVAALE-SABAGAGTLANPLGTLNPLKLLSSGIPVNHLEGSQ 76  
DB 8 AKALLKGVGAPVAEGVAILKVEEAARAKQLPGPLV---VKSQHAGG-----RKKG 57  
QY 77 KCVAGELGPOAVGAVKALKAL 96  
DB 58 K-FKELGPDAGGVRLAKSI 76  
  
RESULT 15  
FXB2\_MOUSE STANDARD; PRT; 428 AA.  
ID FXB2\_MOUSE  
AC Q64733;  
DT 01-NOV-1997 (Rel. 35, Created)  
DT 01-NOV-1997 (Rel. 35, Last sequence update)  
DE 30-MAY-2000 (Rel. 39, Last annotation update)  
DE Forkhead box protein B2 (Transcription factor FKHX-4).  
GN FOXB2 OR FKHX4.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=97014266; PubMed=8861101;  
RA Kaestner K.H., Schuetz G., Monaghan A.P.;  
RT "Expression of the winged helix genes fkh-4 and fkh-5 defines domains  
in the central nervous system.";  
RL Mech. Dev. 55:221-230(1996).  
RN [2]  
RP SEQUENCE OF 4-114 FROM N.A.  
RC STRAIN=129;  
RX MEDLINE=93361500; PubMed=7689224;  
RA Kaestner K.H., Lee K.H., Schloendorff J., Hiemisch H.,  
RA Monaghan A.P., Schuetz G.;  
RT "Six members of the mouse forkhead gene family are developmentally  
regulated.";  
RL Proc. Natl. Acad. Sci. U.S.A. 90:7628-7631(1993).  
CC -1- SUBCELLULAR LOCATION: Nuclear.  
CC -1- DEVELOPMENTAL STAGE: Expressed during embryogenesis.  
CC -1- SIMILARITY: Contains 1 fork-head domain.  
CC  
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CC  
CC EMBL; X92591; CAA63335.1; -;  
DR EMBL; X71942; CAA50744.1; -;  
DR PIR; D47746; D47746.  
DR HGSP; Q63245; 2FEH.  
DR TRANSFAC; T02442; -;  
DR MGD; MGI1347468; Foxb2.  
DR InterPro; IPR001766; TF\_Fork\_head.  
DR Pfam; PF00250; Fork\_head; 1.  
DR PRINTS; PR00053; FORKHEAD.  
DR ProDom; PD000425; TF\_Fork\_head; 1.  
DR SMART; SM00339; FH; 1.  
DR PROSITE; PS00657; FORK\_HEAD\_1; 1.  
DR PROSITE; PS00658; FORK\_HEAD\_2; 1.  
DR PROSITE; PSS0039; FORK\_HEAD\_3; 1.  
DR DNA-binding; Nuclear protein; Transcription regulation.  
FW DNA BIND 12 103  
FT FORK-HEAD.

FT DOMAIN 139 153 POLY-HIS.  
FT DOMAIN 156 162 POLY-HIS.  
FT DOMAIN 163 172 POLY-PRO.  
FT DOMAIN 219 231 POLY-ALA.  
FT DOMAIN 249 258 POLY-ALA.  
FT DOMAIN 321 330 POLY-ALA.  
FT DOMAIN 396 399 POLY-ALA.  
SQ SEQUENCE 428 AA; 45170 MW; DB88BFD1B94AB10 CRC64;  
Query Match 14.1%; Score 71; DB 1; Length 428;  
Best Local Similarity 29.2%; Pred. No. 28;  
Matches 33; Conservative 17; Mismatches 43; Indels 20; Gaps 6;  
QY 11 VALSCSAAFLVGSAPVQA-PVALESAAGAGTLANPLGTINPL-----KL 59  
DB 220 VAAAAAASAAVSGVRLSOFPPYGLSAAAAAASAASTTGKHPAENIIGRDYKG 279  
QY 60 LLSGLGIP-----VNHU---IEGS-QKCVAGLGPVAGVAKKALLGALTVP 104  
DB 280 VLOAGGLPLASVHHLGYPVPGQLSNVGVSMVPH-VGVNDSVAAAAAASAAAG 331  
RESULT 16  
DNAA RHIME STANDARD; PRT; 480 AA.  
AC P35890;  
DT 01-JUN-1994 (Rel. 29, Created)  
DT 16-OCT-2001 (Rel. 40, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Chromosomal replication initiator protein dnaA.  
GN DNAA OR R00368 OR SMC01167.  
OS Rhizobium meliloti (Sinorhizobium meliloti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.  
OX NCBI\_TaxID=382;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=95270610; PubMed=7751302;  
RA Margolin W., Bramhill D., Long S.R.;  
RT "The dnaA gene of Rhizobium meliloti lies within an unusual gene  
arrangement";  
RN J. Bacteriol. 177:2892-2900(1995).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=1021;  
RX MEDLINE=21396507; PubMed=11481430;  
RA Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J.,  
Boistard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S.,  
Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D.,  
Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U.,  
Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.;  
RT "Analysis of the chromosome sequence of the legume symbiont  
Sinorhizobium meliloti strain 1021";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).  
CC -!- FUNCTION: Plays an important role in the initiation and regulation  
of chromosomal replication. Binds to the origin of replication; it  
binds specifically double-stranded DNA at a 9 bp consensus (dnaA  
box): 5'-TTATC(C/A)(C/A)-3'. DnaA binds to ATP and to acidic  
phospholipids.  
CC -!- SIMILARITY: Belongs to the dnaA family.  
CC  
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CC  
CC EMBL; L25439; AAA26258.1; ALT\_INIT.  
DR EMBL; L39265; AAA91097.1; ALT\_INIT.  
DR EMBL; AL591783; CAC41805.1; ALT\_INIT.

DR HAMAP; MF\_00377; -; 1.  
DR InterPro; IPR003593; AAA\_ATPase.  
DR InterPro; IPR001957; Bac\_DnaA.  
DR Pfam; PF00308; bac\_dnaA; 1.  
DR PRINTS; PR00051; DNaA.  
DR SMART; SW00382; AAA; 1.  
DR TIGRFAMs; TIGR00362; DnaA; 1.  
DR PROSITE; PS01008; DNaA; 1.  
KW DNA replication; DNA-binding; ATP-binding; Complete proteome.  
FT NP BIND 181 188 ATP (POTENTIAL).  
SQ SEQUENCE 480 AA; 53579 MW; A346219949FAD6A3 CRC64;  
Query Match 14.1%; Score 71; DB 1; Length 480;  
Best Local Similarity 38.9%; Pred. No. 31;  
Matches 21; Conservative 11; Mismatches 14; Indels 8; Gaps 3;  
QY 20 AFVLSAKVAFVVALESAAAGAGTLANPLGTINPLKLLSLGIPVNHLE 73  
DB 147 SPFVGGSSNRVA-LAAARTIAAGAGAV-----RFNPL-FIHSSVGLGKTHLQ 192  
RESULT 17  
RL7\_RALSO STANDARD; PRT; 124 AA.  
AC Q8KUZ7;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE 50S ribosomal protein L7/L12.  
GN RPL1 OR RSC3035 OR RS04722.  
DB Ralstonia solanacearum (Pseudomonas solanacearum).  
OS Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Burkholderiaceae; Ralstonia.  
OX NCBI\_TaxID=305;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=GMI1000;  
RX MEDLINE=21681879; PubMed=11823852;  
RA Salancoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,  
Arlat M., Billault A., Brottier P., Camus J.C., Cattolico L.,  
Chandler M., Choise N., Claudel-Renard C., Cunnac S., Demange N.,  
Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,  
Sigulier P., Thebault P., Whalen M., Wincker P., Levy M.,  
Weissenbach J., Boucher C.A.;  
RT "Genome sequence of the plant pathogen Ralstonia solanacearum";  
RL Nature 415:497-502(2002).  
CC -!- FUNCTION: Seems to be the binding site for several of the factors  
involved in protein synthesis and appears to be essential for  
accurate translation (By similarity).  
CC -!- SIMILARITY: Belongs to the L12P family of ribosomal proteins.  
CC  
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CC  
CC EMBL; AL646073; CAD16744.1; -.  
DR HAMAP; MF\_00368; -; 1.  
DR InterPro; IPR008932; Ribos\_L12/7\_olig.  
DR InterPro; IPR00206; Ribosomal\_L12.  
DR Pfam; PF00542; Ribosomal\_L12; 1.  
DR ProDom; PD001326; Ribosomal\_L12; 1.  
DR TIGRFAMs; TIGR00855; L12; 1.  
KW Ribosomal protein; Complete proteome.  
SQ SEQUENCE 124 AA; 12520 MW; 271C3CF71F80269E CRC64;  
Query Match 13.7%; Score 69; DB 1; Length 124;  
Best Local Similarity 31.8%; Pred. No. 14;  
Matches 28; Conservative 17; Mismatches 35; Indels 8; Gaps 5;



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DR EMBL; X57471; CAA40707.1; -.
DR EMBL; X59402; CAA42043.1; -.
DR EMBL; AE000164; AAC73691.1; -.
DR EMBL; U82598; AAB40789.1; ALT_INIT.
DR PIR; S16296; S16296.
DR EcoGene; EGI0246; fepD.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF01032; FecCD; 1.
DR ProDom; PD001557; FecCD; 1.
KW Iron transport; Transport; Inner membrane; Transmembrane;
KW Complete proteome.
FT TRANSMEM 10 30 POTENTIAL.
FT TRANSMEM 64 84 POTENTIAL.
FT TRANSMEM 93 113 POTENTIAL.
FT TRANSMEM 121 141 POTENTIAL.
FT TRANSMEM 152 172 POTENTIAL.
FT TRANSMEM 193 213 POTENTIAL.
FT TRANSMEM 240 260 POTENTIAL.
FT TRANSMEM 282 302 POTENTIAL.
FT TRANSMEM 306 326 POTENTIAL.
FT TRANSMEM 334 354 POTENTIAL.
FT TRANSMEM 334 354 POTENTIAL.
SQ SEQUENCE 334 AA; 33871 MW; 8033838090484FC1 CRC64;

Query Match 13.5%; Score 68; DB 1; Length 334;
Best Local Similarity 22.1%; Pred. No. 42;
Matches 34; Conservative 19; Mismatches 43; Indels 58; Gaps 6;

Qy 3 LAALLGLCVALS---SAAFLVGS---KPAQP----- 32
Db 41 LEAFSGTQSADCTIVLDARLPETLAGLGGALGLAGALMOTLRNPLADPGLGVNAG 100
Qy 33 -----VAALSAAGAGAGTIANPL-----GTINPLKILLSSLGIPV 68
Db 101 ASPAIVLGAALFGYSQAQQLANAFAGALVSLIVAFSGSGGQLSPVRLTA--GVAL 158
Qy 69 NHLIEGSKVAGLGFQAVGVKVALIGALTIV 102
Db 159 AAVLEGLTSGIALLNPVVDQLRFQA--GSLDI 190
```

## RESULT 20

```
ID SILF_MOUSE STANDARD; PRT; 569 AA.
AC Q920G3;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Sialic acid binding Ig-like lectin-F precursor (mSilec-F).
GN SIGLEC-F.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RX MEDLINE=21576254; PubMed=11579105;
RA Angata T., Hingorani R., Varki N.M., Varki A.;
RT "Cloning and characterization of a novel mouse Siglec-F:
RT differential evolution of the mouse and human (CD33) Siglec-3-related
RT gene clusters."
RJ J. Biol. Chem. 276:45128-45136 (2001).
CC -!- FUNCTION: Putative adhesion molecule that mediates sialic-acid
CC dependent binding to cells. Preferentially binds to alpha2,3-
CC linked sialic acid. The sialic acid recognition site may be masked
CC by cis interactions with sialic acids on the same cell surface.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- TISSUE SPECIFICITY: Predominantly expressed by immature
CC monocytic/myeloid lineage cells in bone marrow. Also found at
CC lower levels in mature neutrophils and monocytes.
CC -!- DOMAIN: Contains 1 copy of a cytoplasmic motif that is referred
CC to as the immunoreceptor tyrosine-based inhibitor motif (ITIM).
```

```
CC This motif is involved in downmodulation of cellular responses.
CC The phosphorylated ITIM motif binds to the SH2 domain of
CC PTPN6/SHP-1.
CC -!- SIMILARITY: Belongs to the immunoglobulin superfamily. SIGLEC
CC (sialic acid binding Ig-like lectin) family.
CC -!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
CC -!- SIMILARITY: Contains 2 immunoglobulin-like C2-type domains.
CC
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CC
CC EMBL; AF293371; AAL11043.1; -.
CC InterPro; IPR007110; IG-like.
CC InterPro; IPR003598; IG_c2.
CC Pfam; PF00047; IG_2.
CC SMART; SM00408; IGC2; 1.
CC PROSITE; PS50835; IG_LIKE; 2.
KW Cell adhesion; Lectin; Transmembrane; Signal; Glycoprotein;
KW Immunoglobulin domain; Repeat.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 569 SIALIC ACID BINDING IG-LIKE LECTIN-F.
FT DOMAIN 17 439 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 440 460 POTENTIAL.
FT DOMAIN 461 569 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 18 116 IG-LIKE V-TYPE.
FT DOMAIN 139 224 IG-LIKE C2-TYPE 1.
FT DOMAIN 229 324 IG-LIKE C2-TYPE 2.
FT SITE 536 541 ITIM MOTIF.
FT SITE 559 564 SLAM-LIKE MOTIF.
FT DISULFID 35 163 BY SIMILARITY.
FT DISULFID 40 96 BY SIMILARITY.
FT DISULFID 157 206 BY SIMILARITY.
FT DISULFID 265 308 BY SIMILARITY.
FT CARBOHYD 95 95 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 151 151 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 200 200 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 203 203 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 369 369 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 372 372 N-LINKED (GLCNAC. .) (POTENTIAL).
FT CARBOHYD 387 387 N-LINKED (GLCNAC. .) (POTENTIAL).
SQ SEQUENCE 569 AA; 61476 MW; 8033838090484FC1 CRC64;
```

```
Query Match 13.5%; Score 68; DB 1; Length 569;
Best Local Similarity 29.9%; Pred. No. 67;
Matches 26; Conservative 11; Mismatches 38; Indels 12; Gaps 3;
```

```
Qy 3 LAALLGLCVALS---SAAFLVGSAXPVQPVVALESAAZAGAGTIANPLGTINPKLLLS 62
Db 447 LMALLAVCLC-----LIFFTVKVLKKSLKVAATKGNHLAKNPASTINSATSS 497
```

```
Qy 63 --SLGIPV-NHLIEGSKVAGLGPQA 86
```

```
Db 498 NIALGYPIQGHNLNPGSQIQKQPPLA 524
```

## RESULT 21

```
ID Y233_HUMAN STANDARD; PRT; 2035 AA.
AC Q92508;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein KIAA0233.
GN KIAA0233.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
```

RP SEQUENCE FROM N.A.  
RC TISSUE=bone marrow;  
RX MEDLINE=97191544; PubMed=9039502;  
RA Nagase T., Seki N., Ishikawa K.-I., Ohira M., Kawarabayashi Y.,  
Ohara O., Tanaka A., Kotani H., Miyajima N., Nomura N.;  
RT "Prediction of the coding sequences of unidentified human genes. VI.  
The coding sequences of 80 new genes (K1AA0201-K1AA0280) deduced by  
analysis of cDNA clones from cell line KG-1 and brain.";  
RT DNA Res. 3:321-329(1996).  
RL  
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CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
CC  
DR EMBL; D87071; BAAL340.1; --  
KW Hypothetical protein.  
FT DOMAIN 260 264 POLY-GLN.  
FT DOMAIN 265 270 POLY-GLU.  
FT DOMAIN 265 270 POLY-LEU.  
FT DOMAIN 450 453 POLY-LEU.  
FT DOMAIN 618 621 POLY-LEU.  
FT DOMAIN 940 944 POLY-GLU.  
FT DOMAIN 1409 1418 POLY-GLU.  
FT DOMAIN 1487 1490 POLY-ILE.  
FT DOMAIN 1680 1683 POLY-LYS.  
SQ SEQUENCE 2035 AA; 233040 MW; F337E333DFC0CB8 CRC64;  
  
Query Match 13.4%; Score 67.5; DB 1; Length 2035;  
Best Local Similarity 29.2%; Pred No. 2.3e+02;  
Matches 19; Conservative 12; Mismatches 29; Indels 5; Gaps 2;  
  
QY 30 AQPVAALSAFAA--GAGTLANPLGTLNPLKLLSSIGIPV---HLIEGSKQCVAE LGP 84  
Db 1085 SQAEATLPQTEAPNAPSTVSGLGAEPLSSMTDDMGSLSTGYHRSGEAEVTDPG 1144  
  
QY 85 QAVGA 89  
Db 1145 REAGA 1149  
  
RESULT 22  
GCP MYCLE  
ID GCP MYCLE STANDARD; PRT; 351 AA.  
AC P37569; Q49725;  
DT 01-OCT-1994 (Rel. 30, Created)  
DT 15-JUL-1998 (Rel. 36, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Probable O-sialoglycoprotein endopeptidase (EC 3.4.24.57)  
DE (Glycoprotease).  
GN GCP OR M0379 OR U229E OR U1620C OR B229\_C3\_246 OR B1620\_C3\_226.  
OS Mycobacterium leprae.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1769;  
RN (1)  
RP SEQUENCE FROM N.A.  
RA Smith D.R., Robison K.;  
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.  
RN (2)  
RP SEQUENCE FROM N.A.  
RC STRAIN=TN;  
RX MEDLINE=21128732; PubMed=11234002;  
RA Cole S.T., Eiglmier K., Parkhill J., James K.D., Thomson N.R.,  
Wheeler P.R., Honore N., Garnier T., Churcher C., Harris D.,  
Mungall K., Basham D., Brown D., Chillingworth T., Connor R.,  
Davies R.M., Devlin K., Duthoy S., Feltwell T., Fraser A., Hamlin N.,  
Holtroyd S., Hornsby T., Jagels K., Lacroix C., Maclean J., Moule S.,  
Murphy L., Oliver K., Quail M.A., Rajandream M.A., Rutherford K.M.,  
Rutter S., Seeger K., Simon S., Simmonds M., Skelton J., Squares R.,

RA Squares S., Stevens K., Taylor K., Whitehead S., Woodward J.R.,  
Barrell B.G.;  
RT "Massive gene decay in the leprosy bacillus.";  
RL Nature 403:1007-1011(2001).  
RN (3)  
RP SEQUENCE OF 286-351 FROM N.A.  
RX MEDLINE=92374850; PubMed=1354834;  
RA de Wit T.F.R., Bekelle S., Oslang A., Miko T.L., Hermans P.W.M.,  
van Soelingen D., Drijfhout J., Schoeningh R., Janson A.A.M.,  
Thole J.E.R.;  
RT "Mycobacteria contain two groEL genes: the second Mycobacterium  
RT leprae groEL gene is arranged in an operon with groES.";  
RL Mol. Microbiol. 6:1995-2007(1992).  
CC -!- FUNCTION: Could be a metalloprotease.  
CC -!- CATALYTIC ACTIVITY: Hydrolysis of O-sialoglycoproteins; cleaves  
CC 31-Arg--Asp-32 bond in glycophorin A. Does not cleave  
CC unglycosylated proteins, desialylated glycoproteins or  
CC glycoproteins that are only N-glycosylated.  
CC -!- COFACTOR: Zinc (Probable).  
CC -!- SIMILARITY: Belongs to peptidase family M22.  
CC  
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CC  
DR EMBL; U00020; AAA17310.1; ALT SEQ.  
DR EMBL; AL583918; CAC29887.1; --  
DR EMBL; U00015; AAC43226.1; --  
DR PIR; S72817; S72817.  
DR Leproma; M0379; --  
DR MEROPS; M22.UFW; --  
DR InterPro; IPR000905; Peptidase\_M22.  
DR Pfam; PF00814; Peptidase\_M22; 1.  
DR PIRSF; PIRSF004537; OSialGlc\_ptds; 1.  
DR PRINTS; PR00789; OSIALOPTASE.  
DR ProDom; PD002367; peptidase\_M22; 1.  
DR TIGRFAMs; TIGR00329; GCP; 1.  
DR ProSITE; PS01016; GLYCOPROTEASE; 1.  
KW Hydrolase; Metalloprotease; Zinc; Complete proteome.  
FT METAL 124 124 ZINC (POTENTIAL).  
FT METAL 128 128 ZINC (POTENTIAL).  
SQ SEQUENCE 351 AA; 35405 MW; F76A14B739A7BAE4 CRC64;  
  
Query Match 13.3%; Score 67; DB 1; Length 351;  
Best Local Similarity 34.5%; Pred No. 53;  
Matches 29; Conservative 6; Mismatches 39; Indels 10; Gaps 2;  
  
QY 4 AALLGLCVALSASSAAFLVGSAPVAPQVVAALSAFAAGAGTLANPLGTLNPLKLLSS 63  
Db 62 AHLEALGPTIRCALAAGLTGSAKPDV-----VAATIGPLAGALLVGVAAKAYSAA 114  
  
QY 64 LGIP---VNHIEGSKQCVAE LGP 84  
Db 115 WGVFPFVAVNHLGHLAADVYEHGP 138  
  
RESULT 23  
FUNG\_PSESV  
ID FUNG\_PSESV STANDARD; PRT; 464 AA.  
AC Q885V0;  
DT 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Fumarate hydratase class II (EC 4.2.1.2) (Fumarase C).  
GN FUNG-1 OR PSP01731.  
OS Pseudomonas syringae (pv. tomato).  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
OC Pseudomonadaceae; Pseudomonas.  
OX NCBI\_TaxID=323;

SEQUENCE FROM N.A.  
MEDLINE=22834015; PubMed=12928499;  
STRAIN=DC3000;  
BUELL C.R., Joadar V., Lindeberg M., Selenberg J., Paulsen I.T.,  
Guinn M.D., Dodson R.J., Deboy K.T., Durkin A.S., Kolonay J.F.,  
Madupu R., Daugherty S., Brink L., Beanan M.J., Haft D.H.,  
Rau W.C., Davidson T., Zafar N., Zhou L., Liu J., Yuan Q.,  
Khouri H., Fedorova N., Tran B., Russell D., Berry K., Utterback T.,  
Van Aken S.E., Feldblum T.V., D'Ascenzo M., Deng W.-L., Ramos A.R.,  
Alfaro J.R., Cartinhouer S., Chatterjee A.K., Delaney T.P.,  
Lazarowitz S.G., Martin G.B., Schneider D.J., Tang X., Bender C.L.,  
White O., Fraser C.W., Collmer A.,  
"The complete genome sequence of the Arabidopsis and tomato pathogen  
Pseudomonas syringae pv. tomato DC3000.";  
Proc. Natl. Acad. Sci. U.S.A. 100:10181-10186(2003).  
-1- CATALYTIC ACTIVITY: (S)-malate = fumarate + H(2)O.  
-1- PATHWAY: Tricarboxylic acid cycle.  
-1- SUBUNIT: Homotrimer (By similarity).  
-1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).  
-1- SIMILARITY: Belongs to the class-II fumarate / aspartate family.  
Fumarate subfamily.  
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-----  
EMBL; AE016862; AAC55251.1; -  
TIGR; PSPT01731; -  
HAMAP; MF\_00743; -  
InterPro; IPR000362; Fumarate\_lyase.  
InterPro; IPR008948; L-Asparagine-like.  
Pfam; PF00206; lyase 1; 1.  
PRINTS; PR00149; FUMARATE\_LYASE.  
PROSITE; PS00163; FUMARATE\_LYASES; 1.  
ACT SITE 186 186  
Ligase: Tricarboxylic acid cycle, Complete proteome.  
FT BINDING 322 322 SUBSTRATE CARBOXYL (POTENTIAL).  
SEQUENCE 464 AA; 49077 MW; 6B12FF7257FFD2 CRC64;  
-----  
Query Match 13.3%; Score 67; DB 1; Length 464;  
Best Local Similarity 31.3%; Pred. No. 68;  
Matches 31; Conservative 14; Mismatches 36; Indels 18; Gaps 5;  
-----  
QY 2 KLAALLGCVLSCSSAAFLVGSAPVAPVALESAAEAGAGTLANPLGTINPLKLI- 60  
DB 247 ELAALSLGFFVTAPNKFAL-LAGH-----EPLAALSGALKTLTLAGTL---WKIANDRLUG 297  
-----  
QY 61 -----LSSLGIPVNHLEIGSKCVABLGQAVGAKAL 93  
DB 298 SGPRAGLAELVELPANE--PGSSIMPGKVNPTCEALSML 334  
-----  
RESULT 24  
ID TA2R RAT STANDARD; PRT; 341 AA.  
AC P34978;  
DT 01-PEB-1994 (Rel. 28, Created)  
DI 01-PEB-1994 (Rel. 28, Last sequence update)  
DI 01-NOV-1997 (Rel. 35, Last annotation update)  
DE Thromboxane A2 receptor (TXA2-R) (Prostanoid TP receptor) (TXR2).  
GN TBXA2R.  
OS Rattus norvegicus (Rat).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A.  
R STRAIN=Sprague-Dawley; TISSUE=Kidney;

MEDLINE=95362824; PubMed=7635958;  
Abe T., Takeuchi K., Takahashi N., Teutsami E., Taniyama Y., Abe K.;  
"Rat kidney thromboxane receptor: molecular cloning, signal  
transduction, and intrarenal expression localization.";  
J. Clin. Invest. 96:657-664(1995).  
[2]  
SEQUENCE FROM N.A.  
STRAIN=Sprague-Dawley; TISSUE=Brain;  
MEDLINE=95510358; PubMed=7696353;  
Kitanaka J., Hashimoto H., Sugimoto Y., Sawada M., Negishi M.,  
Suzumura A., Marunouchi T., Ichikawa Y., Baba A.;  
"cDNA cloning of a thromboxane A2 receptor from rat astrocytes.";  
Biochim. Biophys. Acta 1265:220-223(1995).  
[3]  
SEQUENCE FROM N.A.  
STRAIN=Sprague-Dawley; TISSUE=Kidney;  
MEDLINE=97090677; PubMed=8936855;  
D'Angelo D.B., Terawata T., Carlisle S.J., Dorn G.W. II, Lynch K.R.;  
"Characterization of a rat kidney thromboxane A2 receptor: high  
affinity for the agonist ligand I-BOP.";  
Prostaglandins 52:303-316(1996).  
-1- FUNCTION: Receptor for thromboxane A2 (TXA2), a potent stimulator  
of platelet aggregation. The activity of this receptor is mediated  
by a G-protein that activate a phosphatidylinositol-calcium second  
messenger system. In the kidney, the binding of TXA2 to glomerular  
TP receptors causes intense vasoconstriction.  
-1- SUBCELLULAR LOCATION: Integral membrane protein.  
-1- TISSUE SPECIFICITY: In the brain, expressed in all types of glial  
cells. In the kidney, expressed in the mesangial cells of the  
glomerulus, smooth muscle cells of the renal arterioles, and in  
transitional cell epithelium of renal pelvis.  
-1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
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-----  
EMBL; D21158; BAA04694.1; -  
PIR; I55623; I55623.  
InterPro; IPR000276; GPCR\_Rhodopsin.  
InterPro; IPR008385; ProstanoidR.  
Pfam; PF00001; 7tm 1; 1.  
PRINTS; PR01788; PROSTANOIDS.  
PROSITE; PS00237; G PROTEIN RECP F1.1; 1.  
PROSITE; PS00262; G PROTEIN RECP F1.2; 1.  
G-protein coupled receptor; Transmembrane; Glycoprotein.  
KW DOMAIN 1 25  
FT TRANSMEM 30 52  
FT DOMAIN 53 65  
FT TRANSMEM 66 86  
FT DOMAIN 87 105  
FT TRANSMEM 106 127  
FT DOMAIN 128 147  
FT TRANSMEM 148 170  
FT DOMAIN 171 191  
FT TRANSMEM 192 217  
FT DOMAIN 218 244  
FT TRANSMEM 245 268  
FT DOMAIN 269 287  
FT TRANSMEM 288 309  
FT DOMAIN 310 341  
FT CARBOHYD 4  
FT CARBOHYD 16  
FT DISULFID 104 181  
FT CONFLICT 188 188  
FT CONFLICT 341 AA;  
SEQUENCE 341 AA; 36927 MW; E85843FE54C1CD94 CRC64;  
-----  
Query Match 13.2%; Score 66.5; DB 1; Length 341;

```

Best Local Similarity 30.2%; Pred. No. 59;
Matches 32; Conservative 11; Mismatches 38; Indels 25; Gaps 5;

QY 8 GLC-VALSCSSAAAFVLSAKPVAQVVALESA-----AAGAGTLANPGLNPLKLL 60
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 115 GLCPILLGAAMAAREVGTIRFSPATSRRAWATVGLVWVGAGTIG-----L 163
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 61 LSLSLGIPVNHLEIGSQKCV-----AELGPOAVGAVKALKKALLGALIV 102
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 164 LPLGLIGRISVQVPGSWCFELTGAERGDVAFG---LMPFALLGSVSV 206
    |||:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 25
FXD1 HUMAN
ID FXD1_HUMAN STANDARD; PRT; 465 AA.
AC Q1676; Q12949;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Forkhead box protein D1 (Forkhead-related protein FKHL8) (Forkhead-
DE related transcription factor 4) (FREAC-4).
GN FOXD1 OR FKHL8 OR FREAC4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96355467; PubMed=8702877;
RA Ernsteason S., Pierrou S., Hulanter M., Cederberg A., Hellqvist M.,
RA Carlsson P., Enerback S.;
RT "Characterization of the human forkhead gene FREAC-4. Evidence for
RT regulation by Wilms' tumor suppressor gene (WT-1) and p53.";
RL J. Biol. Chem. 271:21094-21099(1996).
RN [2]
RP SEQUENCE OF 120-225 FROM N.A.
RX MEDLINE=95045392; PubMed=7957066;
RA Pierrou S., Hellqvist M., Samuelsson L., Enerbaeck S., Carlsson P.;
RT "Cloning and characterization of seven human forkhead proteins:
RT binding site specificity and DNA bending.";
RL EMBO J. 13:5002-5012(1994).
CC -1- FUNCTION: Binding of FREAC-3 and FREAC-4 to their cognate sites
CC results in bending of the DNA at an angle of 80-90 degrees.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- SIMILARITY: Contains 1 fork-head domain.
CC
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CC
CC -----
CC EMBL; U59832; AAC50661.1; -
CC EMBL; U59831; AAC50660.1; -
CC EMBL; U13222; AAA92039.1; -
CC PIR; G02738; G02738.
CC PIR; S51627; S51627.
CC HSP; Q63245; 2HFX.
CC TRANSFAC; T02472; -.
CC Genew; HGNC:3802; FOXD1.
CC MIM; 601091; -.
CC DR GO; GO:0003700; F:transcription factor activity; TAS.
CC DR InterPro; IPR001766; TF_Fork_head.
CC DR Pfam; PF00250; Fork_head; 1.
CC DR PRINTS; PR00053; FORKHEAD.
CC DR ProDom; PD000425; TF_Fork_head; 1.
CC DR SMART; SM00339; FH; 1.
CC DR PROSITE; PS00657; FORK HEAD 1; 1.
CC DR PROSITE; PS00658; FORK HEAD 2; 1.
CC DR PROSITE; PS00659; FORK HEAD 3; 1.
CC DR PROSITE; PS00658; FORK HEAD 3; 1.
CC DR Transcription regulation; DNA-binding; Nuclear protein.

```

```

FT DOMAIN 26 34 POLY-GLU.
FT DOMAIN 39 43 POLY-GLY.
FT DOMAIN 52 57 POLY-ARG.
FT DOMAIN 59 72 POLY-GLU.
FT DOMAIN 73 76 POLY-ASP.
FT DOMAIN 97 113 POLY-GLY.
FT DNA_BIND 124 215 FORK-HEAD.
FT DOMAIN 231 234 POLY-ALA.
FT DOMAIN 252 256 POLY-ALA.
FT DOMAIN 259 266 POLY-PRO.
FT DOMAIN 293 303 POLY-ALA.
FT DOMAIN 309 315 POLY-PRO.
FT DOMAIN 375 390 POLY-ALA.
FT DOMAIN 428 434 POLY-ALA.
SQ SEQUENCE 465 AA; 46140 MW; D3E7854909CCBF AE CRC64;

Query Match 13.2%; Score 66.5; DB 1; Length 465;
Best Local Similarity 28.9%; Pred. No. 76;
Matches 28; Conservative 7; Mismatches 43; Indels 19; Gaps 3;

QY 12 ALSCSSAAAFVLSAKPVAQVVALESAAGAGTLANPGLT--NPKLLLSLGLIP-- 67
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 295 AAAAAAAAFPHSPPPPPPPHGAALARTAFGYRPHPLGALPGPLPASAAKAGGFGA 354
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

QY 68 -----VNHLIEGSKVAVELGPOAVGAVKALKA 95
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|
Db 355 SALASPPSIESIIIGSS-----LGPAAAAAAQA 385
    :|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|:|

RESULT 26
NLTD BRAOL
ID NLTD_BRAOL STANDARD; PRT; 118 AA.
AC Q43304;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Nonspecific lipid-transfer protein D precursor (LTP D) (Wax-associated
DE protein 9D).
DE protein 9D).
GN WAX9D.
OS Brassica oleracea (Cauliflower).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; Core eudicots; Rosids;
OC eurosids II; Brassicales; Brassicaceae; Brassica.
OX NCBI_TaxID=3712;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Leaf.
RX MEDLINE=94263227; PubMed=8203911;
RA Pyee J., Yu H., Kolattukudy P.E.;
RT "Identification of a lipid transfer protein as the major protein in
RT the surface wax of broccoli (Brassica oleracea) leaves.";
RL Arch. Biochem. Biophys. 311:460-468(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Green sprouting; TISSUE=Leaf;
RX MEDLINE=95201828; PubMed=7894511;
RA Pyee J., Kolattukudy P.E.;
RT "The gene for the major cuticular wax-associated protein and three
RT homologous genes from broccoli (Brassica oleracea) and their
RT expression patterns.";
RL Plant J. 7:49-59(1995).
CC -1- FUNCTION: Plant nonspecific lipid-transfer proteins transfer
CC phospholipids as well as galactolipids across membranes. May play
CC a role in wax or cutin deposition in the cell walls of expanding
CC epidermal cells and certain secretory tissues.
CC -1- SIMILARITY: Belongs to the plant LTP family.
CC
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CC  
CC  
DR EMBL; L29767; AAA32995.1; -  
DR EMBL; L33907; AAA73948.1; -  
DR PIR; S45680; S45680.  
DR HSSP; P19656; IMZM.  
DR InterPro; IPR003612; AAI.  
DR InterPro; IPR000528; Plant LTP.  
DR Pfam; PF00234; tryp\_alpha\_amy1; 1.  
DR PRINTS; PR00382; LIPIDTRANSF.  
DR SMART; SM00499; AAI; 1.  
DR PROSITE; PS00597; PLANT\_LTP; 1.  
KW Lipid-binding; Transport; Signal; Multigene family.  
FT SIGNAL 1 25  
FT CHAIN 26 118  
FT DISULFID 29 77  
FT DISULFID 39 54  
FT DISULFID 55 100  
FT DISULFID 75 114  
SQ SEQUENCE 118 AA; 11937 MW; 53214BCDC4491DFC CRC64;  
  
Query Match 13.1%; Score 66; DB 1; Length 118;  
Best Local Similarity 22.7%; Pred. No. 25;  
Matches 25; Conservative 18; Mismatches 35; Indels 32; Gaps 3;  
  
QY 1 MKLAALGLGV-----ALSCSAAAFVLSAKPVAQPVAALESAAEAGAGTL--- 47  
DB 5 MKLAALGLGV-----ALSCSAAAFVLSAKPVAQPVAALESAAEAGAGTL--- 47  
QY 48 -----ANPLGTINPLKL--LLSSLGIPVNHLEGSQRC 78  
DB 65 ARTTPDQQACRCLVGAANALPIINVARAAGLPKACGVNIFYKISTTNC 114  
  
RESULT 27  
MP70 MYCKA STANDARD; PRT; 121 AA.  
ID Q49614;  
AC 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Immunogenic protein MP70 analog precursor (Fragment).  
OS Mycobacterium kansasii.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1768;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NC7C 10268;  
RX MEDLINE=97218684; PubMed=9066106;  
RA Woolford A.J., Hewinson R.G., Woodward M., Dale J.W.;  
RT "Sequence heterogeneity of an mpb70 gene analogue in Mycobacterium kansasii.";  
RL PEMS Microbiol. Lett. 148:43-48(1997).  
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).  
CC -!- SIMILARITY: Contains 1 PAS1 domain.  
CC  
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CC  
CC EMBL; X99760; CAA68089.1; -  
DR InterPro; IPR000782; BIGH3\_FAS1.  
DR Pfam; PF02469; Fasciclin; 1.  
DR PROSITE; PS50213; FAS1; 1.  
Signal.  
FT SIGNAL 1 28  
FT CHAIN 29 >121  
FT DOMAIN 55 >121  
KW POTENTIAL.  
FT SIGNAL 29 >121  
FT CHAIN 55 >121  
FT DOMAIN 55 >121  
KW IMMUNOGENIC PROTEIN MP70 ANALOG.  
FT SIGNAL 29 >121  
FT CHAIN 55 >121  
FT DOMAIN 55 >121

FT NON\_TER 121  
SQ SEQUENCE 121 AA; 11930 MW; AD17BD8C67F537E CRC64;  
  
Query Match 13.1%; Score 66; DB 1; Length 121;  
Best Local Similarity 32.9%; Pred. No. 25;  
Matches 26; Conservative 12; Mismatches 21; Indels 20; Gaps 4;  
  
QY 4 AALLGLCVALSASSAAAFVLSG-----SAKPVAQPVAALESAAEAGAGTLA--NPL--- 51  
DB 13 AAVVGLAVATPTAAADLVGSCADYAAANPSGP--ASVEGMSQVVPVAAASNNPMLTT 70  
QY 52 -----GTLNPLKLLSSSL 64  
DB 71 LTSAVSGRLNPQVNLVDYL 89  
  
RESULT 28  
CLRC IDEDE STANDARD; PRT; 239 AA.  
ID P60000;  
AC 15-MAR-2004 (Rel. 43, Created)  
DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Chlorate reductase gamma subunit precursor (Chlorate reductase heme subunit).  
DE subunit).  
GN CLRC.  
OS Ideonella dechloratans.  
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;  
OC Ideonella.  
OX NCBI\_TaxID=36863;  
RN [1]  
RP SEQUENCE FROM N.A., AND CHARACTERIZATION.  
RA Danielsson Thorell H., Stenflo K., Karlsson J., Nilsson T.;  
RT "A gene cluster for chlorate metabolism in Ideonella dechloratans.";  
RL Appl. Environ. Microbiol. 69:5585-5592(2003).  
CC -!- FUNCTION: May transfer electrons to the iron-sulfur centers of ClrB.  
CC -!- COFACTOR: Binds 1 heme B (iron-protoporphyrin IX) group per molecule (Potential).  
CC -!- SUBUNIT: Heterotrimer of alpha, beta and gamma subunits.  
CC -!- SUBCELLULAR LOCATION: Periplasmic.  
CC -!- BIOTECHNOLOGY: Has potential use in bioremediation of waste sites contaminated with chlorate, such as pulp and paper industry wastewater.  
CC  
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CC  
CC EMBL; AJ566363; CAD97450.1; -  
KW Electron transport; Periplasmic; Heme; Signal.  
FT SIGNAL 1 27  
FT CHAIN 28 239  
FT METAL 74 74  
FT METAL 138 138  
SQ SEQUENCE 239 AA; 25500 MW; DB471B3218ACD5A6 CRC64;  
  
Query Match 13.1%; Score 66; DB 1; Length 239;  
Best Local Similarity 40.0%; Pred. No. 47;  
Matches 20; Conservative 8; Mismatches 18; Indels 4; Gaps 2;  
  
QY 1 MKLAALGLCVALSASSAAAFVLSGAKPVAQPVAALESAAEAGAGTLAMP 50  
DB 7 VKRVAVIGLAAVAACTGAAAGAAAGQ--AVPQAQRIIRVLSVA---GGDAASP 52  
  
RESULT 29  
PTB\_MOUSE STANDARD; PRT; 527 AA.  
ID PTB\_MOUSE

AC P17225;  
DT 01-AUG-1990 (Rel. 15, Created)  
DT 01-AUG-1992 (Rel. 23, Last sequence update)  
DE 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Polypyrimidine tract-binding protein 1 (PTB) (Heterogeneous nuclear  
ribonucleoprotein I) (hnRNP I).  
GN PTBP1 OR PTB.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP MEDLINE=92105132; PubMed=1722210;  
RX Botwell A.L.M., Ballard D.W., Philbrick W.M., Lindwall G.,  
RA Maher S.E., Bridgett M.M., Jamison S.F., Garcia-Blanco M.A.;  
RT "Murine polypyrimidine tract binding protein. Purification, cloning,  
RT and mapping of the RNA binding domain.";  
RL J. Biol. Chem. 266:24657-24663 (1991).  
CC -!- FUNCTION: Plays a role in pre-mRNA splicing. Binds to the  
CC polypyrimidine tract of introns. May promote the binding of U2  
CC snRNP to pre-mRNA.  
CC -!- SUBUNIT: Part of a ternary complex containing FUBP2, PTBP1, PTBP2  
CC and HNRPH1 (By similarity).  
CC -!- SUBCELLULAR LOCATION: Nuclear.  
CC -!- DOMAIN: The C-terminal 195 amino acids of PTB are sufficient for  
CC specific RNA binding.  
CC -!- SIMILARITY: Contains 4 RNA recognition motif (RRM) domains.  
CC  
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CC  
CC EMBL; X52101; CAA36321.1;  
DR MGD; MG1:97791; Ptbp1.  
DR GO; GO:0005634; C:nucleus; IDA.  
DR InterPro; IPR006536; HNRNP-L\_PTB.  
DR InterPro; IPR000504; RNA\_rec\_mot.  
DR Pfam; PF00076; rtm; 4.  
DR SMART; SM00360; RRM; 3.  
DR TIGRFAMs; TIGR01649; hnRNP-L\_PTB; 1.  
DR PROSITE; PS0102; RRM; 4.  
DR PROSITE; PS00030; RRM\_RNP\_1; FALSE NEG.  
KW Nuclear protein; RNA-binding; mRNA splicing; Repeat.  
FT DOMAIN 58 142 RNA-BINDING (RRM) 1.  
FT DOMAIN 183 259 RNA-BINDING (RRM) 2.  
FT DOMAIN 335 386 RNA-BINDING (RRM) 3.  
FT DOMAIN 450 525 RNA-BINDING (RRM) 4.  
FT DOMAIN 315 321 POLY-ALA.  
SQ SEQUENCE 527 AA; 56478 MW; F18FDF376010D76A CRC64;  
Query Match 13.1%; Score 66; DB 1; Length 527;  
Best Local Similarity 26.7%; Pred. No. 94;  
Matches 31; Conservative 16; Mismatches 37; Indels 32; Gaps 4;  
QY 12 ALSGSSAAAF-----LVGSAKPVAOPVAALSAE-----AGAGTLANPLGTINPLK 58  
DB 287 SLDQWAAAFGLSVNVHGALAPLAPGAAAAAASRAIPGLAGAGNSVLLVNLNPER 346  
QY 59 LILSLGI-----FVNLIEGSKQVAVELG--PQAVGAVKAKA 95  
DB 347 VTFQSLFILFGVYGVQVRVKILFNKENALVQMDGSAQLGEPERAAAREVSA 402  
RESULT 30  
LEUL\_PROMM STANDARD; PRT; 540 AA.  
ID LEUL\_PROMM  
AC Q7UTV5;  
DT 15-MAR-2004 (Rel. 43, Created)

DT 15-MAR-2004 (Rel. 43, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE 2-isopropylmalate synthase (EC 2.3.3.13) (Alpha-isopropylmalate  
synthase) (Alpha-IPM synthetase).  
GN LEUA OR PWT121  
OS Prochlorococcus marinus (strain MIT 9313).  
OC Bacteria; Cyanobacteria; Prochlorophytes; Prochlorococcaceae;  
OC Prochlorococcus.  
OX NCBI\_TaxID=74547;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22825698; PubMed=12917642;  
RA Rocap G., Larimer F.W., Lamerdin J., Malfatti S., Chain P.,  
RA Ahlgren N.A., Bellano A., Coleman M., Hauser L., Hees W.R.,  
RA Johnson Z.I., Land M., Lindell D., Post A.F., Regala W., Shah M.,  
RA Shaw S.L., Steglich C., Sullivan S.B., Ting C.S., Tolonen A.,  
RA Webb E.A., Zinser E.R., Chisholm M.W.;  
RT "Genome divergence in two Prochlorococcus ecotypes reflects oceanic  
RT niche differentiation.";  
RL Nature 424:1042-1047 (2003).  
CC -!- FUNCTION: Catalyzes the condensation of the acetyl group of  
CC acetyl-CoA with 3-methyl-2-oxobutanoate (2-oxoisovalerate) to form  
CC 3-carboxy-3-hydroxy-4-methylpentanoate (2-isopropylmalate).  
CC -!- CATALYTIC ACTIVITY: Acetyl-CoA + 3-methyl-2-oxobutanoate + H(2)O =  
CC 2-hydroxy-2-isopropylsuccinate + CoA.  
CC -!- PATHWAY: Leucine biosynthesis; first step.  
CC -!- SUBUNIT: Homotrimer (By similarity).  
CC -!- SIMILARITY: Belongs to the alpha-IPM synthetase / homocitrate  
CC synthase family. Leua 1 subfamily.  
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CC  
CC EMBL; BX572098; CAE21296.1;  
DR HAMAP; MF\_01025; -;  
DR InterPro; IPR002034; AIPM/Hcit\_synth.  
DR InterPro; IPR000891; HMGL-like\_synth.  
DR InterPro; IPR005871; Leua\_bact\_synth.  
DR Pfam; PF00682; HMGL-like; 1.  
DR TIGRFAMs; TIGR00973; leua\_bact; 1.  
DR PROSITE; PS00816; AIPM\_HOMOCIT\_SYNTH\_1; 1.  
DR PROSITE; PS00816; AIPM\_HOMOCIT\_SYNTH\_2; 1.  
KW Leucine biosynthesis; Transferase; Complete proteome.  
SQ SEQUENCE 540 AA; 57970 MW; A68C19587E8FE7DE CRC64;  
Query Match 13.1%; Score 66; DB 1; Length 540;  
Best Local Similarity 32.5%; Pred. No. 96;  
Matches 26; Conservative 10; Mismatches 34; Indels 10; Gaps 3;  
QY 11 VALSCSSAAAFVGSAPVAPVAALSAEAGAGTLANPLGTINPLKLLSSIGIPVNH 70  
DB 412 VQVSCGS-----SLRPTATVILAQEDGQEQTAAVGT--GPVDVAVCRNALAGEPNE 462  
QY 71 LTGSKQCVAVELGPQAVGAV 90  
DB 463 LTFRSVKSVTE-GIDANGEV 481  
RESULT 31  
NUP1\_RAT STANDARD; PRT; 585 AA.  
ID NUP1\_RAT  
AC P70581; Q9CHE1; Q9QWK7; Q9Z2W7;  
DT 10-OCT-2003 (Rel. 42, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Nucleoporin p58/p45 (Nucleoporin-like protein 1).  
GN NUP1.  
OS Rattus norvegicus (Rat).

CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
OX NCBI\_TaxID=10116;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM P58), SEQUENCE OF 227-237; 317-333;  
RP 403-422 AND 427-433, ALTERNATIVE SPLICING. FUNCTION: SUBCELLULAR  
RP LOCATION, IDENTIFICATION IN A COMPLEX WITH NUP62 AND NUP54, AND  
RP INTERACTION WITH NUPF2.  
RP TISSUE=Macrophage;  
RX MEDLINE=96326666; PubMed=8707840;  
RA Hu T., Guan T., Gerace L.;  
RT "Molecular and functional characterization of the p62 complex, an  
RT assembly of nuclear pore complex glycoproteins.";  
RL J. Cell Biol. 134:589-601 (1996).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS P45 AND P23), SEQUENCE OF 309-585 FROM  
RP N.A. (ISOFORM H6), AND TISSUE SPECIFICITY.  
RP TISSUE=Macrophage;  
RX MEDLINE=99013879; PubMed=9795236;  
RA Hu T., Gerace L.;  
RT "cDNA cloning and analysis of the expression of nucleoporin p45.";  
RL Gene 221:245-253 (1998).  
CC -!- FUNCTION: Component of the nuclear pore complex, a complex  
CC required for the trafficking across the nuclear membrane.  
CC -!- SUBUNIT: Component of the p62 complex, a complex composed of  
CC NUP62, NUP54, and the isoform p58 and isoform p45 of NUP1.  
CC Isoform p58 interacts with NUPF2. Isoform p58 interacts with SRP1-  
CC alpha and Importin p97 proteins when they are together, but not  
CC with SRP1-alpha protein alone.  
CC -!- SUBCELLULAR LOCATION: Central region of the nuclear pore complex,  
CC within the transporter. Localizes on both cytoplasmic and  
CC nucleoplasmic sides of the nuclear pore complex near the central  
CC gated channel.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=4;  
CC Name=p58;  
CC IsoId=P70581-1; Sequence=Displayed;  
CC Name=p45;  
CC IsoId=P70581-2; Sequence=VSP\_008579, VSP\_008580, VSP\_008581;  
CC Name=p23;  
CC IsoId=P70581-3; Sequence=VSP\_008576, VSP\_008577, VSP\_008578,  
CC VSP\_008582;  
CC Note=No experimental confirmation available;  
CC Name=H6;  
CC IsoId=P70581-4; Sequence=VSP\_008583, VSP\_008584;  
CC Note=No experimental confirmation available;  
CC -!- TISSUE SPECIFICITY: Expressed in liver.  
CC -!- DOMAIN: Contains F-G repeats.  
CC -!- PTM: O-glycosylated.  
CC -!- SIMILARITY: Belongs to the NUP1 family.  
CC  
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CC  
CC EMBL; U63839; AAC52789.1; -  
DR EMBL; AF000898; AAC82539.1; -  
DR EMBL; AF000900; AAC82318.1; -  
DR EMBL; AF000901; AAC82319.1; -  
KW Transport; Nuclear protein; Repeat; Coiled coil; Glycoprotein;  
KW Alternative splicing.  
FT DOMAIN 7 565 14 X 2 AA REPEATS OF F-G.  
FT REPEAT 7 8 1.  
FT REPEAT 30 31 2.  
FT REPEAT 42 43 3.  
FT REPEAT 61 62 4.  
FT REPEAT 66 67 5.  
FT REPEAT 242 262  
FT DOMAIN 300 367 COILED COIL (POTENTIAL).  
FT COILED COIL (POTENTIAL).

FT REPEAT 474 475 6.  
FT REPEAT 478 479 7.  
FT REPEAT 499 500 8.  
FT REPEAT 505 506 9.  
FT REPEAT 515 516 10.  
FT REPEAT 517 518 11.  
FT REPEAT 531 532 12.  
FT REPEAT 554 555 13.  
FT REPEAT 564 565 14.  
FT VARSPLIC 328 337  
PADYFRVLVQ -> SPDDERLQVH (in isoform  
p23).  
FT VARSPLIC 466 468 /FTID=VSP\_008576.  
FT VARSPLIC 469 585 /FTID=VSP\_008577.  
FT VARSPLIC 224 245 /FTID=VSP\_008578.  
FT VARSPLIC 531 535 /FTID=VSP\_008579.  
FT VARSPLIC 536 585 /FTID=VSP\_008580.  
FT VARSPLIC 1 327 /FTID=VSP\_008581.  
FT VARSPLIC 466 471 /FTID=VSP\_008582.  
FT VARSPLIC 472 585 /FTID=VSP\_008583.  
FT VARSPLIC 585 AA; 59265 MW; 4DSF5C2744A75C3C CRC64;  
SQ SEQUENCE 13.1%; Score 66; DB 1; Length 585;  
Query Match 27.5%; Pred. No. 1e-02; Mismatches 11; Gaps 4;  
Best Local Similarity 30; Conservative 48; Indels 20;  
Matches 30; Mismatches 48; Indels 20; Gaps 4;  
QY 12 ALSCSAAAFVLVG-----SAKPVAPQV-----AALESAAEAGAGTLANPLGTL 54  
Db 85 ATTSASTTGSLGFSKPAASATFPALPTVTTASGLTSSALTSPASTGTNNLGA- 143  
QY 55 NPULKLLSSIGIPVNHLEGSQKVAELGPQAVGAV--KALKALIGALT 101  
Db 144 TPATTTAASTGLSLGALAGLGGSLFQSGNTATSGLGQNALSLSLGTAT 192  
RESULT 32  
EUTC\_RHOER STANDARD; PRT; 257 AA.  
ID EUTC\_RHOER  
AC Q53782;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 28-FEB-2003 (Rel. 41, Last annotation update)  
DE Ethanolamine ammonia-lyase light chain (EC 4.3.1.7) (Ethanolamine  
DE ammonia-lyase small subunit).  
GN EUTC.  
OS Rhodococcus erythropolis.  
OS Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Nocardiaceae; Rhodococcus.  
OX NCBI\_TaxID=1833;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NI86/21;  
RX MEDLINE=94349216; PubMed=8069783;  
RA De Mot R., Nagy I., Schoofs G., Vanderleyden J.;  
RT "Sequence of Rhodococcus gene cluster encoding the subunits of  
RT ethanolamine ammonia-lyase and an APC-like permease.";  
RL Can. J. Microbiol. 40:403-407 (1994).  
CC -!- CATALYTIC ACTIVITY: Ethanolamine = acetaldehyde + NH(3).  
CC -!- COFACTOR: Adenosylcobalamin.  
CC -!- PATHWAY: Ethanolamine utilization.  
CC -!- SUBUNIT: Heterodimer of a small and a large subunit (By  
CC similarity).  
CC -!- SIMILARITY: Belongs to the eutC family.  
CC  
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-----

CC EMBL; L24492; AAC37137.1; -;  
DR HAMAP; MF 00601; -; 1.  
SQ SEQUENCE 257 AA; 26963 MW; E6E3FA138F49C91B CRC64;

Query Match 13.0%; Score 65.5; DB 1; Length 257;  
Best Local Similarity 25.3%; Pred. No. 55;  
Matches 25; Conservative 18; Mismatches 41; Indels 15; Gaps 4;  
QY 17 SAAFLVGSAAKPVQAPVALES-----AAAGAGTLANPLGTUNPKLLLSLGIPIV 68  
DB 130 SALVTALGERSYAPPIVATNARVALGDHIAAGVQTAIVLIGE-RPGLSVADSVGIYL 188  
QY 69 NHL-----IEGSKQVABL-GPQAVGAVKALKALLGALT 101  
DB 189 THLPVGVTDADRNCSINVHPPEGLGYEQARVVVLGLVT 227

RESULT 33  
COBT\_RHILO STANDARD; PRT; 336 AA.  
AC Q98K9; 30-MAY-2000 (Rel. 39, Created)  
DT 10-OCT-2003 (Rel. 42, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Nicotinate-nucleotide-dimethylbenzimidazole phosphoribosyltransferase  
DE (EC 2.4.2.21) (NN:DBI PRT) (N(1)-alpha-phosphoribosyltransferase).  
GN COBT OR MUR1389.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MAFP303099;  
RX MEDLINE=21082930; PubMed=11214968;

RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Ideawake K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
RT Mesorhizobium loti".  
RL DNA Res. 7:331-338(2000).  
CC -!- FUNCTION: Catalyzes the synthesis of alpha-ribazole-5'-phosphate  
CC from nicotinate mononucleotide (NAMN) and 5,6-  
CC dimethylbenzimidazole (DMB).  
CC -!- CATALYTIC ACTIVITY: Beta-nicotinate D-ribonucleotide +  
CC dimethylbenzimidazole = nicotinate + N(1)-(5-phospho-alpha-D-  
CC ribosyl)-5,6-dimethylbenzimidazole.  
CC -!- PATHWAY: Cobalamin biosynthesis.  
CC -!- SIMILARITY: Belongs to the cobt family.  
-----

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CC EMBL; AP002997; BAB48775.1; -;  
DR HSSP; Q05603; 1DGS.  
DR HAMAP; MF 00230; -; 1.  
DR InterPro; IPR003200; NN:DBI\_PRT.  
DR InterPro; IPR008281; NN:DBI\_PRT\_sub.

DR Pfam; PF02277; DBI\_PRT; 1.  
DR ProDom; PD009438; NN:DBI\_PRT; 1.  
KW Cobalamin biosynthesis; Porphyrin biosynthesis; Transferase;  
KW Glycosyltransferase; Complete proteome.  
FT ACT SITE 304 BASE (BY SIMILARITY).  
SQ SEQUENCE 336 AA; 34408 MW; F9824D6693745932 CRC64;

Query Match 13.0%; Score 65.5; DB 1; Length 336;  
Best Local Similarity 26.9%; Pred. No. 70;  
Matches 35; Conservative 12; Mismatches 44; Indels 39; Gaps 5;  
QY 7 LGCVLSCSSAAAFVLSGAK-----PVAPVALESAAEAGAGTLANPLGTUN 55  
DB 164 IGNTTAAATSAALFGGAEKMTGRGTGVDAGLKRKVVAIEAGLKRHAALADPLGVA 223  
QY 56 PL-----KLLLSLGIPIVNLIEGSKQCVAEI GPQA-----VGAV 90  
DB 224 ALGRELALFAGTALARHLGIPV--LLDGF-VCTRAAPLARLHPTGLSHITIAHVSNE 280  
QY 91 KALKALIGAL 100  
DB 281 SGHRLLEAL 290

RESULT 34  
Y084\_MYCTU STANDARD; PRT; 491 AA.  
AC O53209; 30-MAY-2000 (Rel. 39, Created)  
DT 30-MAY-2000 (Rel. 39, Last sequence update)  
DT 10-OCT-2003 (Rel. 42, Last annotation update)  
DE Hypothetical protein RV2484C/MY2555.  
GN RV2484C OR MY2557 OR MYV008.40C.  
OS Mycobacterium tuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Mycobacteriaceae; Mycobacterium.  
OX NCBI\_TaxID=1773;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=H37RV;  
RX MEDLINE=96295987; PubMed=9634230;

RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,  
RA Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekala F.,  
RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,  
RA Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Holroyd S.,  
RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,  
RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,  
RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,  
RA Sulston J.E., Taylor K., Whitehead S., Barrall B.G.;  
RT "Deciphering the biology of Mycobacterium tuberculosis from the  
RT complete genome sequence".  
RL Nature 393:537-544(1998).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=CDC 1551 / Oshkosh;  
RX MEDLINE=22206494; PubMed=12218036;

RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,  
RA Peterson J., DeBoy R., Dodson R., Gwinn M., Haft D., Hickey E.,  
RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M., Salzberg S.L.,  
RA Decher A., Utterback T., Weidman J., Khouri H., Gill J., Mikula A.,  
RA Bishai W., Jacobs W.R. Jr., Venter J.C., Fraser C.M.;  
RT "Whole-genome comparison of Mycobacterium tuberculosis clinical and  
RT laboratory strains".  
RL J. Bacteriol. 184:5479-5490(2002).

CC -!- SIMILARITY: Belongs to the UPF0089 family.  
-----  
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CC EMBL; AL021246; CAA16061.1; --
DR EMBL; AE007092; AAK46861.1; --
DR PIR; C70868; C70868.
DR TIGR; WT2557; --
DR Tuberculin; RV2484c; --
DR InterPro; IPR004255; UPF0089.
DR Pfam; PF03007; UPF0089; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 491 AA; 52309 MW; C2ACC8458ADF82DD CRC64;

Query Match 13.0%; Score 65.5; DB 1; Length 491;
Best Local Similarity 36.7%; Pred. No. 98;
Matches 22; Conservative 8; Mismatches 23; Indels 7; Gaps 2;

QY 4 AALLGLCVALSASSAAFLVGSAPVQVVAALSAEAGAG-----TLNPLGTINPL 57
DB 281 AVLAGLIGALRYHEALGVPISTLPMVAV-NLRAEGDAGGNOFTGVNLAAPVGTIDPV 339

RESULT 35
TRD2_RALSO STANDARD; PRT; 344 AA.
AC O8XS00;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Anthranilate phosphoribosyltransferase 2 (EC 2.4.2.18).
GN TRPD2 OR RSP0691 OR RS01768.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Plasmid megaplasmid.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GM11000;
RX MEDLINE=21691879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brotigier P., Camus J.C., Cattolico L.,
RA Chandler M., Choine N., Claudel-Renard C., Cunnac S., Demange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RA "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
CC -1- CATALYTIC ACTIVITY: Anthranilate + phosphoribosyldiphosphate =
CC N-5'-phosphoribosyl-anthranilate + diphosphate.
CC -1- PATHWAY: Tryptophan biosynthesis; second step.
CC -1- SIMILARITY: Belongs to the anthranilate phosphoribosyltransferase
CC family.
CC
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CC
CC EMBL; AL646080; CAD17832.1; --
DR HANAP; MF_00211; -- 1
DR InterPro; IPR005940; Ant_phospho_trans.
DR InterPro; IPR000312; Glyco_transf_3.
DR Pfam; PF02885; Glycos_transf_3N; 1.
DR Pfam; PF00591; Glycos_transf_3; 1.
DR ProDom; PD001864; Glyco_transf_3; 1.
DR ProDom; PD001864; Glyco_transf_3; 1.
DR TIGRfam; TIGR01245; trpd; 1.
KW Tryptophan biosynthesis; Transferase; Glycosyltransferase; Plasmid;
KW Complete proteome.
SQ SEQUENCE 344 AA; 35977 MW; 65074865254E2F2 CRC64;

Query Match 12.9%; Score 65; DB 1; Length 344;
```

```
Best Local Similarity 27.6%; Pred. No. 79;
Matches 27; Conservative 18; Mismatches 29; Indels 24; Gaps 5;

QY 16 SSSAAFLV-GSAKPVQVVAALSAEAGAGTIANPLGTINPLKLLSSLGIPVNHILG 74
DB 93 STCAAFIVAGAGVEV-----AKHGNRALSSKSGAAD-----VLSALGVNLDQTPAD 138

QY 75 SQKQVRELG-----PQAVGAVKALKAL-----LGALTIVF 103
DB 139 IERCIAEAGIGFMFAPTHHPALKQLMPVRVDLATRIIF 176

RESULT 36
YM56_SYNBL
ID YM56_SYNBL STANDARD; PRT; 399 AA.
AC Q8DGR0;
DT 10-OCT-2003 (Rel. 42, Created)
DT 10-OCT-2003 (Rel. 42, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Hypothetical UPF0272 protein t112296.
GN T112296.
OS Synecococcus elongatus (Thermosynechococcus elongatus).
OC Bacteria; Cyanobacteria; Chroococcales; Synecococcus.
OX NCBI_TaxID=32046;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BP-1;
RX MEDLINE=2225144; PubMed=12240834;
RA Nakamura Y., Kaneko T., Sato S., Ikeuchi M., Katoh H., Sasamoto S.,
RA Watanabe A., Iriguchi M., Kawashima K., Kimura T., Kishida Y.,
RA Kiyokawa C., Kohara M., Matsumoto M., Matsuno A., Nakazaki N.,
RA Shimo S., Sugimoto M., Takeuchi C., Yamada M., Tabata S.;
RA "Complete genome structure of the thermophilic cyanobacterium
RA Thermosynechococcus elongatus BP-1.";
RL DNA Res. 9:123-130(2002).
CC -1- SIMILARITY: Belongs to the UPF0272 family.
CC
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CC
CC EMBL; AF005376; BAC09848.1; --
DR HANAP; MF_01074; -- 1.
DR InterPro; IPR002822; DUF111.
DR Pfam; PF01969; DUF111; 1.
DR ProDom; PD018127; DUF111; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 399 AA; 43522 MW; 9742A63BD0C9CE12 CRC64;

Query Match 12.9%; Score 65; DB 1; Length 399;
Best Local Similarity 34.0%; Pred. No. 90;
Matches 34; Conservative 10; Mismatches 34; Indels 22; Gaps 7;

QY 12 ALSCSAAFLVGSAPVQVVAALSAEAGAGTIANPLGTINPLKLLSSLGIPVNHIL 71
DB 200 ALVCAUSAGF-----GAPPANTLQRVG-LGAGTQELPLNL--LRMLGTVPAPPE-- 247

QY 72 IEQSQKQVREL-----GPQAVG-AVKALKALGLTIVF 103
DB 248 -TGTAKTIVELOTQLDDMPFQALSACEOLVA-AGALEVF 285

RESULT 37
AZAC_HUMAN
ID AZAC_HUMAN STANDARD; PRT; 462 AA.
AC P18825; P35369; Q9HB49;
DT 01-NOV-1990 (Rel. 16, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
```

[illegible]

RL J. Bacteriol. 173:6837-6843 (1991).  
RP (2)  
RN SEQUENCE FROM N.A.  
RC STRAIN-K12;  
RA MEDLINE=92184121; PubMed=1544582;  
RX Kaiman M., Murphy H., Cashel M.,  
RT "The nucleotide sequence of recG, the distal spo operon gene in  
RL Escherichia coli K-12";  
RN Gene 110:95-99 (1992).  
RP (3)  
RN SEQUENCE FROM N.A.  
RC STRAIN-K12 / MG1655;  
RA MEDLINE=93315143; PubMed=7668882;  
RX Burland V.D., Plunkett G. III, Daniels D.L., Blattner F.R.;  
RT "DNA sequence and analysis of 136 kilobases of the Escherichia coli  
RL genome: organizational symmetry around the origin of replication";  
RN Genomics 16:551-561 (1993).  
RP (4)  
RN FUNCTION.  
RC MEDLINE=95045415; PubMed=7957087;  
RX Whitby M.C., Vincent S.D., Lloyd R.G.;  
RA "Branch migration of Holliday junctions: identification of RecG  
RL protein as a junction specific DNA helicase";  
RN EMBO J. 13:5220-5228 (1994).  
RP (5)  
RN FUNCTION.  
RC MEDLINE=95292979; PubMed=7774596;  
RX Hong X., Cadwell G.W., Kogoma T.;  
RA "Escherichia coli RecG and RecA proteins in R-loop formation.";  
RL EMBO J. 14:2385-2392 (1995).  
CC -!- FUNCTION: Critical role in recombination and DNA repair. Help  
CC process Holliday junction intermediates to mature products by  
CC catalyzing branch migration. Has a DNA unwinding activity  
CC characteristic of a DNA helicase with a 3' to 5' polarity. recG  
CC unwind branched duplex DNA (Y-DNA). Has a role in constitutive  
CC stable DNA replication (cdR) and R-loop formation.  
CC -!- SIMILARITY: Belongs to the helicase family. RecG subfamily.  
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CC  
CC EMBL; X59550; CAA42123.1; -  
CC EMBL; M64367; AAR24513.1; -  
CC EMBL; L10328; AAR62005.1; -  
CC EMBL; AB000442; AAC76676.1; -  
CC PIR; JH0265; JH0265.  
CC EcoGene; EG10829; recG.  
CC InterPro; IPR001410; DEAD.  
CC InterPro; IPR001650; Helicase\_C.  
CC InterPro; IPR008994; Nucleic\_acid\_OB.  
CC InterPro; IPR004509; RecG.  
CC InterPro; IPR004365; trna\_anti.  
CC Pfam; PF00270; DEAD; 1.  
CC Pfam; PF00271; helicase\_C; 1.  
CC Pfam; PF01336; trna\_anti; 1.  
CC Pfam; PF00487; DEXDC; 1.  
CC SMART; SM00490; HELIC; 1.  
CC SMART; SM00490; HELIC; 1.  
CC TIGRfam; TIGR00643; recG; 1.  
KW Hydroxylase; Helicase; DNA repair; ATP-binding; DNA recombination;  
FT DNA-binding; Complete proteome.  
FT NP\_BIND 296 303 ATP (POTENTIAL).  
FT SITE 397 400 DEQH BOX.  
FT SEQUENCE 693 AA; 76430 MW; 7826143A8F4292A2 CRC64;  
Query Match 12.9%; Score 65; DB 1; Length 693;  
Best Local Similarity 30.2%; Pred.No. 1.5e+02;  
Matches 26; Conservative 10; Mismatches 44; Indels 6; Gaps 2;

QY 23 VGSAPKPAQVVAALSAEAGAGTLANPLGTL-----NPLKLLSLSLGIPVNHLEGSQK 77  
Db 298 VSGKTIIVAAALAAIAHAGKQVALMAPTELLAAQHANNFNWFAPLGIEVGWL-AGKQK 356  
QY 78 CVAELGPQAVGAVKALKALLGALTIVF 103  
Db 357 GKARLAQQEAIASGOVQMTIVGTGTHAIF 382  
RESULT 39  
ANK3 HUMAN  
ID -ANK3\_HUMAN STANDARD; PRT; 4377 AA.  
AC Q12955;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 15-MAR-2004 (Rel. 43, Last annotation update)  
DE Ankyrin 3 (ANK-3) (Ankyrin G).  
GN ANK3.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Brain stem;  
RX MEDLINE=95138209; PubMed=7836469;  
RA Kordeli B., Lambert S., Bennett V.;  
RT "AnkyrinG, A new ankyrin gene with neural-specific isoforms localized  
RL at the axonal initial segment and node of Ranvier";  
RJ J. Biol. Chem. 270:2352-2359 (1995).  
CC -!- FUNCTION: Membrane-cytoskeleton linker. The neural-specific  
CC isoforms may participate in the maintenance/targeting of ion  
CC channels and cell adhesion molecules at the nodes of Ranvier and  
CC axonal initial segments.  
CC -!- SUBUNIT: Neural-specific isoforms may be a constituent of a  
CC neurofascin/NRCAM/ankyrin G complex.  
CC -!- ALTERNATIVE PRODUCTS:  
CC Event-Alternative splicing; Named isoforms=1;  
CC Comment=A number of isoforms are produced;  
CC Name=1; Synonyms=480-kDa isoform;  
CC IsoId=Q12955.1; Sequence=Displayed;  
CC -!- TISSUE SPECIFICITY: Expressed in brain and other tissues. Isoform  
CC 1 is neural-specific.  
CC -!- SIMILARITY: Contains 23 ANK repeats.  
CC -!- SIMILARITY: Contains 1 death domain.  
CC  
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CC  
CC EMBL; U13616; AAA64834.1; -  
CC PIR; A55575; A55575.  
CC HSP; P55273; 1B18.  
CC Genew; HGNC:494; ANK3.  
CC MIM; 600485; -  
CC GO; GO:0006605; P:protein targeting; NAS.  
CC InterPro; IPR002110; ANK.  
CC InterPro; IPR000488; Death.  
CC InterPro; IPR000906; ZUS.  
CC Pfam; PF00023; ank; 24.  
CC Pfam; PF00531; death; 1.  
CC Pfam; PF00791; ZUS; 1.  
CC PRINTS; PR01415; ANKYRIN.  
CC SMART; SM00248; ANK; 21.  
CC SMART; SM00005; DEATH; 1.  
CC SMART; SM00218; ZUS; 1.  
CC PROSITE; PS50088; ANK\_REPEAT; 21.  
CC PROSITE; PS50297; ANK\_REPEAT\_REGION; 1.  
CC PROSITE; PS50017; DEATH\_DOMAIN; 1.

```

KW Cytoskeleton; Alternative splicing; Repeat; ANK repeat.
FT REPEAT 73 102 ANK 1.
FT REPEAT 106 135 ANK 2.
FT REPEAT 139 168 ANK 3.
FT REPEAT 172 201 ANK 4.
FT REPEAT 203 230 ANK 5.
FT REPEAT 234 263 ANK 6.
FT REPEAT 267 296 ANK 7.
FT REPEAT 300 329 ANK 8.
FT REPEAT 333 362 ANK 9.
FT REPEAT 365 395 ANK 10.
FT REPEAT 399 428 ANK 11.
FT REPEAT 432 461 ANK 12.
FT REPEAT 465 494 ANK 13.
FT REPEAT 498 527 ANK 14.
FT REPEAT 531 560 ANK 15.
FT REPEAT 564 593 ANK 16.
FT REPEAT 597 626 ANK 17.
FT REPEAT 630 659 ANK 18.
FT REPEAT 663 692 ANK 19.
FT REPEAT 696 725 ANK 20.
FT REPEAT 729 758 ANK 21.
FT REPEAT 762 791 ANK 22.
FT REPEAT 795 825 ANK 23.
FT REPEAT 828 857 ANK 24.
FT DOMAIN 1519 1898 SER-RICH.
FT DOMAIN 4030 4174 DEATH.
SQ SEQUENCE 4377 AA; 480399 MW; F42379B55768B684 CRC64;

Query Match 12.9%; Score 65; DB 1; Length 4377;
Best Local Similarity 26.2%; Pred. No. 7.7e+02;
Matches 27; Conservative 17; Mismatches 35; Indels 24; Gaps 4;

QY 16 SAAAPLVGSAKFAVQAQVAA---LESAEAGAGCTLANPL-----GTLNPLK 58
DB 1665 TSAAPLSSPLKSVVSVKSRVDVSSAKITWASLSLSPVKMPGHAEVALVNGSISPLK 1724
QY 59 LLLSLGIPVNHLEIGSKQVAEIQPQAVGAVKAKALLGALT 101
DB 1725 YASSST-----LINGC-KATATLQEKISSATNSVSSVSAAT 1760

RESULT 40
CYCM BRAJA
ID CYCM BRAJA STANDARD; PRT; 184 AA.
AC P30323;
DT 01-APR-1993 (Rel. 25, Created)
DT 01-APR-1993 (Rel. 25, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Cytochrome c homolog.
GN CYCM OR BR1423.
OS Bradyrhizobium japonicum.
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Bradyrhizobiaceae; Bradyrhizobium.
OX NCBI_TaxID=375;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=USDA 110spc4;
RX MEDLINE=92041558; PubMed=1657867;
RA Bott M., Ritz D., Hennecke H.;
RT "The Bradyrhizobium japonicum cycM gene encodes a membrane-anchored
homolog of mitochondrial cytochrome c."
RN [2]
RL J. Bacteriol. 173:6766-6772(1991).

SEQUENCE FROM N.A.
RC STRAIN=USDA 110;
RX MEDLINE=22484998; PubMed=12597275;
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,
RA Sasamoto S., Watanabe A., Ideawa K., Iiguchi M., Kawashina K.,
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,
RA Tabata S.;
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium
Bradyrhizobium japonicum USDA110."
RL DNA Res. 9:189-197(2002).

```

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CC -!- FUNCTION: MAY BE INVOLVED IN ELECTRON TRANSFER FROM B-C1 COMPLEX
CC TO AA3.
CC -!- SUBCELLULAR LOCATION: Type II membrane protein.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL Outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL; M77189; AAA26198.1; -.
CC DR EMBL; AF005940; BAC4688.1; -.
CC DR PIR; A41331; A41331.
CC DR HSSP; P00004; 1WEJ.
CC DR InterPro; IPR003088; Cyt_C1.
CC DR InterPro; IPR002327; Cyt_C1AB.
CC DR InterPro; IPR000345; CytC_heme_BS.
CC DR Pfam; PF00034; cytochrome_c_1.
CC DR PRINTS; PR00604; CYTCRMECIAB.
CC DR PRODOM; PD000375; Cyt_C1AB; 1.
CC DR PROSITE; PS00190; CYTOCHROME_C; 1.
CC DR Electron transport; Heme; Transmembrane; Signal-anchor;
KW Complete proteome.
PT DOMAIN 1 10 CYTOPLASMIC (POTENTIAL).
PT TRANSMEM 11 31 SIGNAL-ANCHOR (POTENTIAL).
PT DOMAIN 32 184 PERIPLASMIC (POTENTIAL).
PT BINDING 84 84 HEME (COVALENT) (BY SIMILARITY).
PT BINDING 87 87 HEME (COVALENT) (BY SIMILARITY).
PT METAL 88 88 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
PT METAL 151 151 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
SQ SEQUENCE 184 AA; 19098 MW; 25CDCAF564389824 CRC64;

Query Match 12.8%; Score 64.5; DB 1; Length 184;
Best Local Similarity 26.9%; Pred. No. 50;
Matches 28; Conservative 14; Mismatches 39; Indels 23; Gaps 5;

QY 3 LAALGLCTVALSCSSAAAFVGSAPVAQP---VALESAA---EAGAGTLANPLGLNLP 56
DB 10 LGAVLGTCLILLVTSFTANALFSPKPEKGFIAVKEDAGHGKGGAAAAAS-----EP 64
QY 57 LKLLSLGIPVNHLEIGSKQVAA-----ELGPQAVGAV 90
DB 65 IEKLQATASVEKG--AAAANKGAGCTFEKGGFNRVGNLYGVV 106

Search completed: April 5, 2004, 14:34:35
Job time : 19 secs

```

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2004, 14:28:38 ; Search time 39 Seconds  
(without alignments)  
841.382 Million cell updates/sec

Title: US-09-997-428-408

Perfect score: 502

Sequence: 1 MKLAALLGLCVALSASSAA.....QAVGAVKALKALIGALTVEG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1017041 seqs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 100 summaries

Database :

- 1: sp\_archaea:\*
- 2: sp\_bacteria:\*
- 3: sp\_fungi:\*
- 4: sp\_human:\*
- 5: sp\_invertebrate:\*
- 6: sp\_mammal:\*
- 7: sp\_mbc:\*
- 8: sp\_organelle:\*
- 9: sp\_phage:\*
- 10: sp\_plant:\*
- 11: sp\_rodent:\*
- 12: sp\_virus:\*
- 13: sp\_vertebrate:\*
- 14: sp\_unclassified:\*
- 15: sp\_rvirus:\*
- 16: sp\_bacteriaph:\*
- 17: sp\_archaeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	225	44.8	94	11	Q8CJC6 mus musculus
2	88	17.5	255	16	Q82LN6
3	83.5	16.6	281	16	Q8F5T3
4	82.5	16.4	247	16	Q9K3G4
5	82.5	16.4	694	16	Q98CR1
6	81	16.1	496	10	Q9SU83
7	80	15.9	148	16	Q8XW23
8	79	15.7	136	16	Q82P50
9	77.5	15.4	229	16	Q7WJ66
10	77.5	15.4	229	16	Q7WJ34
11	77.5	15.4	229	16	Q7VVA1
12	77.5	15.4	601	16	Q86691
13	77	15.3	453	17	Q8TH10
14	76	15.1	355	16	Q8UAI4
15	76	15.1	699	16	Q9ABL0
16	76	15.1	889	16	Q8G4X4

90 69.5 13.8 387 16 Q88L86  
91 69.5 13.8 396 16 Q8RVR2  
92 69.5 13.8 409 16 Q8Y2W6  
93 69.5 13.8 423 16 Q7U114  
94 69.5 13.8 426 16 Q05907  
95 69.5 13.8 427 2 Q9FB37  
96 69.5 13.8 455 16 Q8ZNL3  
97 69.5 13.8 455 16 Q8Z599  
98 69.5 13.8 495 16 Q8NTN6  
99 69.5 13.8 567 16 Q9SM48  
100 69.5 13.8 636 16 Q8SQ7

ALIGNMENTS

RESULT 1  
Q8CUC6 PRELIMINARY; PRT; 94 AA.  
AC Q8CUC6  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE UGRP2 type B.  
GN SCGB3A1.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22326074; PubMed=12438750;  
RA Niimi T., Copeland N.G., Gilbert D.J., Jenkins N.A., Srisodsai A.,  
RA Zimonic D.B., Keck-Weggoner C.L., Popescu N.C., Kimura S.,  
RT "Cloning, expression, and chromosomal localization of the mouse gene  
RT (Scgb3a1, alias Ugrp2) that encodes a member of the novel uteroglobin-  
RT related protein gene family."  
RL Cytogenet. Genome Res. 97:120-127 (2002).  
DR EMBL: AF313457; AAN62328.1; -.  
DR MGI:1915912; SCGB3A1.  
SQ SEQUENCE 94 AA; 9578 MW; 7C84B908A6365B59 CRC64;

Query Match 44.8%; Score 225; DB 11; Length 94;  
Best Local Similarity 57.3%; Pred. No. 2e-13;  
Matches 51; Conservative 14; Mismatches 20; Indels 4; Gaps 2;  
QY 17 SAAFLVGSAPVAPVAALSAEAGAGTLAN-PLGTLPKLLSLGIPVNHLEGS 75  
DB 9 SVAFMDSLAPVAPVAPVAALAPAAEAVAGVPSLPPLSHLALRFLASMGIPDLPLIEGS 68  
QY 76 QKCVAGLPQAVGAVKALKALGALTVEG 104  
DB 69 RKCVTGLGPEAVGAV---KSLGLVLTWFG 94

RESULT 2  
Q82LN6 PRELIMINARY; PRT; 255 AA.  
AC Q82LN6  
DT 01-JUN-2003 (TrEMBLrel. 24, Created)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Putative methionine aminopeptidase.  
GN SAV1974.  
OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomyces; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=33903;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,

Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osone T.,  
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
RT "Genome sequence of an industrial microorganism Streptomyces  
RT avermitilis: deducing the ability of producing secondary  
RT metabolites.";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220 (2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RX STRAIN=WA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=22608306; PubMed=12692562;  
RA Ikeda H., Ishikawa J., Hanamoto A., Shinose M., Kikuchi H., Shiba T.,  
RA Sakaki Y., Hattori M., Omura S.;  
RT "Complete genome sequence and comparative analysis of the industrial  
RT microorganism Streptomyces avermitilis.";  
RL Nat. Biotechnol. 21:528-531 (2003).  
DR EMBL: AP005029; BAC69685.1; -.  
DR GO: GO:0004239; F:metionyl aminopeptidase activity; IEA.  
DR GO: GO:0008508; P:proteolysis and peptidolysis; IEA.  
DR InterPro: IPR000994; Peptidase M24.  
DR InterPro: IPR002467; Pept M24A\_MAP1.  
DR InterPro: IPR001714; Pept\_M24\_MAP.  
DR Pfam: PF00557; Peptidase M24; 1.  
DR PRINTS; PR00599; NAPEPTIDASE.  
DR TIGRFAMs; TIGR00500; met\_pase\_I; 1.  
KW Aminopeptidase; Complete proteome.  
SQ SEQUENCE 255 AA; 26727 MW; 0C41CD3010F855A3 CRC64;  
Query Match 17.5%; Score 88; DB 16; Length 255;  
Best Local Similarity 31.6%; Pred. No. 2.7;  
Matches 31; Conservative 16; Mismatches 19; Indels 32; Gaps 6;  
QY 7 LGICVA---LSCSSAAFLVGSAPVAPVALE-----SAAAGA--GTLANPL 51  
DB 99 LDLAVAGGVAAADAISFLVGKARP-ABSVMATEATERALAAGIAAKFGARIGDLSHAI 157  
QY 52 GTLNPLKLLSLGIPVNHLEGSQKVAELGPQAVGA 89  
DB 158 GT-----VLKAGYYPIN-----TEFGHGIGS 179  
RESULT 3  
Q8FST3 PRELIMINARY; PRT; 281 AA.  
AC Q8FST3  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)  
DE Conserved hypothetical protein.  
GN CE0299.  
OS Corynebacterium efficiens.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxID=152794;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX STRAIN=YS-314 / AJ 12310 / DSM 44549 / JCM 11189;  
RA Kawabayashi Y., Yamazaki J., Hino Y., Kikuchi H., Nakamura Y.,  
RA Ikeo K., Suzuki M., Mashima J., Itoh T., Yamagishi A., Nishio Y.,  
RA Usuda Y., Sugimoto S.;  
RT "The entire genomic sequence of Corynebacterium efficiens YS-314.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL: AP005215; BAC17109.1; -.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 281 AA; 28188 MW; 3143B69C35048C2D CRC64;  
Query Match 16.8%; Score 83.5; DB 16; Length 281;  
Best Local Similarity 30.1%; Pred. No. 7.7;  
Matches 40; Conservative 9; Mismatches 45; Indels 39; Gaps 7;  
QY 3 LAALLGLCV-----ALSCSSAAFLVGSAPVAPVALESAAE-----AGAGTL 47  
DB 106 LAGFLGLICGNLRAGAPMADMDHALHTTGTSGAGTTTVALTAARRVRSGGSGAAVL 165

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QY 48 ANP-----LGTL-----NPKLLSLSGIPVNHLEIGS-----QKQVAF-EPQAV 87
:      :      :      :      :      :      :      :      :      :
Db 166 IDAPMDQLRGTIVESEHGIPVRLDQL-----KRLAEQHRHQASAAQLOQPOAT 221
:      :      :      :      :      :      :      :      :      :
QY 88 GAVKALKALLGAL 100
:      :      :      :      :      :      :      :      :      :
Db 222 AVILLALLPLAGVL 234
:      :      :      :      :      :      :      :      :      :

RESULT 4
Q9K3G4 PRELIMINARY; PRT; 247 AA.
AC Q9K3G4
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TReMBLrel. 23, Last annotation update)
DE Hypothetical protein SC01277.
GN SC01277 OR 2SG18.24.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D.; Chater K.F.; Cerdano-Tarraga A.-M.; Challis G.L.;
RA Thomson N.R.; James K.D.; Harris D.E.; Quail M.A.; Kieser H.;
RA Harper D.; Bateman A.; Brown S.; Chandra G.; Chen C.W.; Collins M.;
RA Cronin A.; Fraser A.; Goble A.; Hidalgo J.; Hornsby T.; Howarth S.;
RA Huang C.-H.; Kieser T.; Larke L.; Murphy L.; Oliver K.; O'Neill S.;
RA Rabinowitz E.; Rajandream M.A.; Rutherford K.; Rutter S.;
RA Seeger K.; Saunders D.; Sharp S.; Squares R.; Squares S.; Taylor K.;
RA Warren T.; Wietzorrek A.; Woodward J.; Barrrell B.G.; Parkhill J.;
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939108; CAB99157.1; -.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 247 AA; 22950 MW; EB32ABD76146881B CRC64;

Query Match 16.4%; Score 82.5; DB 16; Length 247;
Best Local Similarity 31.8%; Pred. No. 8.3;
Matches 34; Conservative 10; Mismatches 40; Indels 23; Gaps 5;

QY 17 SAAAFVLSAKP-----VAOPVVALESABAG-----AGTLANPLGT-----NPKL 59
:      :      :      :      :      :      :      :      :      :
Db 61 NALALAGAVNPATLAGVTPPLAALGCGAGNPLAGLAGAGPLONTAGAAQNPLAA 120
:      :      :      :      :      :      :      :      :      :

QY 60 LLSL--GIPVNHLEIGSKQVAFEPQAVGAVKALKALGALTFFG 104
:      :      :      :      :      :      :      :      :      :
Db 121 LTGAAGGNPLAALGGAGNPLAALG-----GAANPLAAGVGAAGALG 163
:      :      :      :      :      :      :      :      :      :

RESULT 5
Q9BCR1 PRELIMINARY; PRT; 694 AA.
AC Q9BCR1
DT 01-OCT-2001 (TReMBLrel. 18, Created)
DT 01-OCT-2001 (TReMBLrel. 18, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Hypothetical protein mlr5043.
GN MLR5043.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NAFF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T.; Nakamura Y.; Sato S.; Asamizu E.; Kato T.; Sasamoto S.;

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RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabata S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti ";
RL DNA Res. 7:331-338(2000).
DR EMBL; AP003005; BAB51560.1; -.
DR GO; GO:000524; F:ATP binding; IEA.
DR GO; GO:0003824; F:catalytic activity; IEA.
DR GO; GO:0004812; F:rRNA ligase activity; IEA.
DR GO; GO:0006418; P:amino acid activation; IEA.
DR GO; GO:0008152; P:metabolism; IEA.
DR InterPro; IPR003781; CoA-binding.
DR InterPro; IPR003611; CoA_ligase.
DR InterPro; IPR001412; tRNA-synt_1.
DR Pfam; PF02629; CoA-binding; 1.
DR PROSITE; PS00178; AA TRNA LIGASE I; 1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 694 AA; 73126 MW; 19E4978531DCF6CC CRC64;

Query Match 16.4%; Score 82.5; DB 16; Length 694;
Best Local Similarity 33.3%; Pred. No. 25;
Matches 33; Conservative 11; Mismatches 42; Indels 13; Gaps 4;

QY 3 LAALLGLCVLSCSSAAAFVLS-APVAPQVVALESAAEAGAGTLANPLGTLP-----L 57
:      :      :      :      :      :      :      :      :      :
Db 438 MVPLFGISEANDAGAAAFICGAWAEFQAQPVDT--SAAGAAG-----GHVTPDEAEA 489
:      :      :      :      :      :      :      :      :      :

QY 58 KLLSSLGIPVNHLEIGSKQVAFEPQAVGAVKALKAL 96
:      :      :      :      :      :      :      :      :      :
Db 490 KARLIKAGLPVPKGERAGNAVEAVISSMALGFPVALKAL 528
:      :      :      :      :      :      :      :      :      :

RESULT 6
Q9SU83 PRELIMINARY; PRT; 496 AA.
AC Q9SU83
DT 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE Nucleotide pyrophosphatase-like protein (EC 3.6.1.9).
GN T16L4.190 OR AT4G29680.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsi.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Bevan M., Rose M., Hempel S., Entian K.-D., Bancroft I., Mewes H.W.,
RA Mayer K.F.X., Lemcke K., Schueller C.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL079344; CAB45328.1; -.
DR EMBL; AL161575; CAB79726.1; -.
DR PIR; T09931; T09931.
DR GO; GO:0016787; F:hydrolase activity; IEA.
DR GO; GO:0004551; F:nucleotide diphosphatase activity; IEA.
DR GO; GO:0009117; P:nucleotide metabolism; IEA.
DR InterPro; IPR002591; Phosphodiester.
DR Pfam; PF01663; Phosphodiester; 1.

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Query Match	15.4%;	Score	77.5;	DB	16;	Length	229;
Best Local Similarity	32.0%;	Pred. No.	22;				

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Matches 32; Conservative 15; Mismatches 30; Indels 23; Gaps 4;
QY 11 VALSCSSAAFLVGSAPVQFVALESAAEAGAGTLANPLGTLNPKLLLSLGIPTVNH 70
Db 144 VQAALASAAAFVGAALPLAIAAA-----PLAQLMPVVIAGSVAGLIGL 189
QY 71 LIEGSKQCVAGLGPQAV-----GAVKALKALLGALTVEG 104
Db 190 AV-AARAGGAPVGAARVVLGAAALTAGVAGAL--FG 226

RESULT 10
Q7WA34 PRELIMINARY; PRT; 229 AA.
AC Q7WA34;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative membrane protein.
GN BP1556
OS Bordetella parapertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebailha M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leathewell S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders S., Stevens K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640427; CA336858.1; --
KW Complete proteome.
SQ SEQUENCE 229 AA; 22750 MW; 5A04498C4875195F CRC64;

Query Match 15.4%; Score 77.5; DB 16; Length 229;
Best Local Similarity 32.0%; Pred. No. 22;
Matches 32; Conservative 15; Mismatches 30; Indels 23; Gaps 4;
QY 11 VALSCSSAAFLVGSAPVQFVALESAAEAGAGTLANPLGTLNPKLLLSLGIPTVNH 70
Db 144 VQAALASAAAFVGAALPLAIAAA-----PLAQLMPVVIAGSVAGLIGL 189
QY 71 LIEGSKQCVAGLGPQAV-----GAVKALKALLGALTVEG 104
Db 190 AV-AARAGGAPVGAARVVLGAAALTAGVAGAL--FG 226

RESULT 11
Q7VVA1 PRELIMINARY; PRT; 229 AA.
AC Q7VVA1;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Putative membrane protein.
GN BP1449.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.

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RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebailha M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdeno-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holtroyd S., Jagels K.,
RA Leathewell S., Moule S., Norberczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders S., Stevens K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica.";
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640415; CA41739.1; --
KW Complete proteome.
SQ SEQUENCE 229 AA; 22776 MW; 5A1EF22D43DFA2FE CRC64;

Query Match 15.4%; Score 77.5; DB 16; Length 229;
Best Local Similarity 32.0%; Pred. No. 22;
Matches 32; Conservative 15; Mismatches 30; Indels 23; Gaps 4;
QY 11 VALSCSSAAFLVGSAPVQFVALESAAEAGAGTLANPLGTLNPKLLLSLGIPTVNH 70
Db 144 VQAALASAAAFVGAALPLAIAAA-----PLAQLMPVVIAGSVAGLIGL 189
QY 71 LIEGSKQCVAGLGPQAV-----GAVKALKALLGALTVEG 104
Db 190 AV-AARAGGAPVGAARVVLGAAALTAGVAGAL--FG 226

RESULT 12
O86691 PRELIMINARY; PRT; 601 AA.
AC O86691;
DT 01-NOV-1998 (TrEMBLrel. 08, Created)
DT 01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Putative transport system permease protein.
GN SC06645 OR SC4G2.19.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomycineae; Streptomycetaceae; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;
RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.P., Cerdeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
DR EMBL; AL939128; CAA20556.1; --
DR PIR; T35054; T35054.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000515; BPD_transp.
DR Pfam; PF00528; BPD_transp; 2.
KW Complete proteome.
SQ SEQUENCE 601 AA; 61216 MW; 78601FC5AB2DCB9C CRC64;

Query Match 15.4%; Score 77.5; DB 16; Length 601;
Best Local Similarity 30.7%; Pred. No. 63;

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Matches 42; Conservative 10; Mismatches 48; Indels 37; Gaps 4;
Qy 3 LAALLGLCVALLSCSSAAAFVLSA--KPVA-----QPVALESAAEAGAG----- 45
Db 426 LVALLVTAVAGSAAATPALAVGAVAWAPAAHTSSLLRQERATLHTATKGLGAGPVHLL 485
Qy 46 -----TLANPLGTINPLKILLSLGI-----PVNHLIEGSKCVAAELGPQ 85
Db 486 RHELLFANVPVVRHALLRLPGVALALASUGFLGLCAQPPSPFWGULLAENQPAERAPW 545
Qy 86 AVGAVKALKALGALTIV 102
Db 546 AVLAPAAVALLGALAV 562

RESULT 13
Q8THLO PRELIMINARY; PRT; 453 AA.
AC Q8THLO;
DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein MA4504.
GN MA4504.
OS Methanosarcina acetivorans.
OC Archaea; Euryarchaeota; Euryarchaeota orders incertae sedis;
OC Methanosarcinales; Methanosarcinaceae; Methanosarcina.
CX NCBI_TaxID=2214;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C2A / ATCC 35395 / DSM 2834;
RX MEDLINE=21929760; PubMed=11932238;
RA Galagan J.E., Nusbaum C., Roy A., Endrizzi M.G., Macdonald P., Brown A.,
RA FitzHugh W., Calvo S., Engels R., Smirnov S., Atroor D., Johnson R.,
RA Allen N., Maylor J., Stange-Thomann N., DeArellano K., Johnson R.,
RA Linton L., McKernan J., Talamas J., Tirrell A., Ye W.,
RA Zimmer A., Barber R.D., Cann I., Graham D.E., Graham D.A., Guss A.M.,
RA Hedderich R., Ingram-Smith C., Kuetner H.C., Krzycki J.A.,
RA Leigh J.A., Li W., Liu J., Mukhopadhyay B., Reeve J.N., Smith K.,
RA Springer T.A., Umayal L.A., White O., White R.H., de Macario E.C.,
RA Ferry J.G., Jarrell K.F., Jing H., Macario A.J.L., Paulsen I.,
RA Pritchett M., Sowers K.R., Swanson R.V., Zinder S.H., Lander E.,
RA Metcalf W.W., Birren B.;
RT "The genome of Methanosarcina acetivorans reveals extensive metabolic
RT and physiological diversity.";
RL Genome Res. 12:532-542(2002).
DR EMBL; AE011170; AAM07844.1; -.
DR GO; GO:0004590; F:orotidine-5'-phosphate decarboxylase activity; IEA.
DR GO; GO:0006207; P:'de novo' pyrimidine base biosynthesis; IEA.
DR InterPro; IPR005493; Methyltransf_6.
DR Pfam; PF03737; Methyltransf_6; 1.
DR Pfam; PF00215; OMPdecase; 1.
DR Hypothetical protein; Complete proteome.
SQ SEQUENCE 453 AA; 48593 MW; 4863027BB4AEA65D CRC64;

Query Match 15.3%; Score 77; DB 17; Length 453;
Best Local Similarity 27.8%; Pred. No. 52;
Matches 30; Conservative 20; Mismatches 34; Indels 24; Gaps 4;
Qy 11 VALSCSSAAAFVLSGAKPVAQPVAALESAAEAGAGTLANPLGTINPLK--LLLSLGI-- 66
Db 102 MAAKAGADVAILIGSADD-STILDALRSAAHKYGVVWADLISAPEPIKRAVDLEALGV 160
Qy 67 -----PVNHLIEGSKCVAAEL-----GFQAVGAVKALKA 95
Db 161 INVHVGIDQVMQKDPISILMEISEKVSQVLAVAGGLDAEGRKAKVKA 208

RESULT 14
Q8UA14 PRELIMINARY; PRT; 355 AA.
AC Q8UA14;

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DT 01-JUN-2002 (TrEMBLrel. 21, Created)
DT 01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE ABC transporter, membrane spanning protein.
GN AFU3389 OR AGR_L_2865.
OS Agrobacterium tumefaciens (strain C58 / ATCC 33970).
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
OC Rhizobiaceae; Rhizobium/Agrobacterium group; Agrobacterium.
CX NCBI_TaxID=176299;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608550; PubMed=11743193;
RA Wood D.W., Setubal J.C., Kaul R., Monks D.E., Kitajima J.P.,
RA Okura V.K., Zhou Y., Chen L., Wood G.E., Almeida N.F. Jr., Woo L.,
RA Chen Y., Paulsen I.T., Eisen J.A., Karp P.D., Bovee D. Sr.,
RA Chapman P., Clendenning J., Deatherage G., Gillet W., Grant C.,
RA Kutayavin T., Levy R., Li M.-J., McLelland E., Palmieri A.,
RA Raymond C., Rouse G., Saenphimmachak C., Wu Z., Romero P., Gordon D.,
RA Zhang S., Yoo H., Tao Y., Biddle P., Jung M., Krespan W., Perry M.,
RA Gordon-Kamm B., Liao L., Kim S., Hendrick C., Zhao Z.-Y., Dolan M.,
RA Chumley F., Tingey S.V., Tomb J.-P., Gordon M.P., Olson M.V.,
RA Neeter E.W.;
RT "The genome of the natural genetic engineer Agrobacterium tumefaciens
RT C58.";
RL Science 294:2317-2323(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21608551; PubMed=11743194;
RA Goodner B., Hinkle G., Gattung S., Miller N., Blanchard M., Mullin L.,
RA Quorillo B., Goldman B.S., Cao Y., Askenazi M., Halling C., Liu F.,
RA Houmiel K., Gordon J., Vaudin M., Iatchouk O., Epp A., Liu F.,
RA Wollam C., Allinger M., Doughty D., Scott C., Lappas C., Markelz B.,
RA Flanagan C., Crowell C., Gurson J., Lomo C., Sear C., Strub G.,
RA Cielo C., Slater S.;
RT "Genome sequence of the plant pathogen and biotechnology agent
RT Agrobacterium tumefaciens C58.";
RL Science 294:2323-2328(2001).
DR EMBL; AE009269; AAL44202.1; -.
DR EMBL; AS008343; AAK90001.1; -.
DR PIR; AD32973; AD2973.
DR PIR; G98309; G98309.
DR GO; GO:0016020; C:membrane; IEA.
DR GO; GO:0005215; P:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR000522; FecD.
DR Pfam; PF01032; FecD; 1.
DR ProDom; PD001557; FecD; 1.
DR Complete Proteome.
KW Complete Proteome.
SQ SEQUENCE 355 AA; 37384 MW; 171A63B72224006C CRC64;

Query Match 15.1%; Score 76; DB 16; Length 355;
Best Local Similarity 23.3%; Pred. No. 49;
Matches 28; Conservative 22; Mismatches 42; Indels 28; Gaps 3;
Qy 2 KLAALLGLCVALLSCSSAAAFVLSGAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLL 61
Db 24 RILVLGLFALCFGNAADMALGPARYTLSEVLA-----TIADPAVGNQLRVVI 73
Qy 62 SSLIGIPVNH-----IEGSKCVA-----ELGPAVGAVKALKALGALTIV 103
Db 74 WDIRMFIAMVTVGASLSVAGAQMTILSNPLASPFITLISAAASFGAALALVGVAIF 133

RESULT 15
Q9ABLO PRELIMINARY; PRT; 699 AA.
AC Q9ABLO;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Thio:disulfide interchange protein, putative.
GN CC0217.
OS Caulobacter crescentus.

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OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;  
 OC Caulobacteraceae; Caulobacter.  
 OX NCBI\_TaxID=155892;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=21173698; PubMed=11259647;  
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,  
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Ely B.,  
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.L., Haft D.H.,  
 RA Kolonay J.P., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
 RA Uterback T., Tran K., Wolf A., Vamathevan J., Emolaeava M., White O.,  
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 RT "Complete genome sequence of *Caulobacter crescentus*,"  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).  
 DR EMBL; AB005696; AAK22204.1; -;  
 DR PIR; H87275; H87275.  
 DR TIGR; CC0217; -;  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0005489; P:electron transporter activity; IEA.  
 DR GO; GO:0007004; P:cyclochrome biogenesis; IEA.  
 DR GO; GO:0006118; P:electron transport; IEA.  
 DR InterPro; IPR003834; Cytococh\_TM.  
 DR InterPro; IPR006663; Thioresox\_dom2.  
 DR Pfam; PF02683; DsbD; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 699 AA; 70749 MW; 6523FSCA7E88B943 CRC64;  
 Query Match 15.1%; Score 76; DB 16; Length 699;  
 Best Local Similarity 30.5%; Pred. No. 1e+02;  
 Matches 32; Conservative 18; Mismatches 37; Indels 18; Gaps 5;  
 QY 3 LAALGLCVALSCTSAALFLVGSAPVAPVAALESAAEAGAGTLANPLGTLPKLL 61  
 Db 545 VSMILGLAVGALAAASLSAKP---PVAAEASTPSGPGTAE---AWSPEKVAL 598  
 QY 62 SSLGIPVNHLEIGS-----QKVAELQPVAVGAVKALKALL 97  
 Db 599 QAEGRPI--LVDFTAWCVCQVNEKVALSGPKVAAEAFKAQNAV 641  
 RESULT 16  
 Q8G4X4  
 ID Q8G4X4 PRELIMINARY; PRT; 889 AA.  
 AC Q8G4X4;  
 DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Protease of ClpA/ClpB type.  
 GN CLPB OR BLI250.  
 OS Bifidobacterium longum.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;  
 OC Bifidobacteriaceae; Bifidobacterium.  
 OX NCBI\_TaxID=216816;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=NCC 2705;  
 RX MEDLINE=22294977; PubMed=12381787;  
 RA Scheil M.A., Karmirantzou M., Snel B., Vilanova D., Berger B.,  
 RA Pessi G., Zwaalen M.-C., Desiere F., Bork P., Delley M.,  
 RA Pridmore R.D., Arigoni F.;  
 RT "The genome sequence of *Bifidobacterium longum* reflects its adaptation  
 RT to the human gastrointestinal tract,"  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).  
 DR EMBL; AS014751; AAN25051.1; -;  
 DR GO; GO:0005524; F:ATP binding; IEA.  
 DR GO; GO:0003754; F:chaperone activity; IEA.  
 DR GO; GO:000166; F:nucleotide binding; IEA.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR003593; AAA\_ATPase.  
 DR InterPro; IPR001270; Chaprinin\_clpA/B.  
 DR InterPro; IPR004176; Clp\_N.

DR Pfam; PF00004; AAA; 2.  
 DR PRINTS; PR00300; CLPPROTEASEA.  
 DR SMART; SMO0382; AAA; 2.  
 DR PROSITE; PS00870; CLPAB\_1; 1.  
 DR PROSITE; PS00871; CLPAB\_2; 1.  
 KW Complete proteome.  
 SQ SEQUENCE 889 AA; 96313 MW; 704B8380EDA2A33C CRC64;  
 Query Match 15.1%; Score 76; DB 16; Length 889;  
 Best Local Similarity 25.7%; Pred. No. 1.3e+02;  
 Matches 26; Conservative 21; Mismatches 36; Indels 18; Gaps 4;  
 QY 16 SSSAAFLVGSAPVAPVAALESAAEAGAGTLANPLGTLPKLL 63  
 Db 497 AEASKILYGEIPTSQKELAAESADASASANPAD--EPWVPDRVDSVAEIVSDM 554  
 QY 64 LGIPVNHLEIGSQKVAE---LGPQVAVKALKALLGL 100  
 Db 555 TGIPVGRIMQGENEKLHLMEDYLGKRVIGQKEIAAASDAV 595  
 RESULT 17  
 Q9F2L6  
 ID Q9F2L6 PRELIMINARY; PRT; 459 AA.  
 AC Q9F2L6;  
 DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
 DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
 DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
 DE Putative integral membrane protein.  
 GN SC03765 OR SCH63.12C.  
 OS Streptomyces coelicolor.  
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
 OC Streptomyces; Streptomycetaceae; Streptomyces.  
 OX NCBI\_TaxID=1902;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Oliver K., Harris D.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;  
 RL Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2);  
 RX MEDLINE=97000351; PubMed=8843436;  
 RA Redenbach M., Kieser H.M., Denapate D., Eichner A., Cullum J.,  
 RA Kinashi H., Hopwood D.A.;  
 RT "A set of ordered cosmids and a detailed genetic and physical map for  
 RT the 8 Mb *Streptomyces coelicolor* A3(2) chromosome,"  
 RL Mol. Microbiol. 21:77-96(1996).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=A3(2) / M145;  
 RX MEDLINE=21996410; PubMed=12000953;  
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,  
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,  
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,  
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,  
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,  
 RA Rabinowitch E., Rajandream M.A., Rutherford K., Rutter S.,  
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,  
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,  
 RA Hopwood D.A.;  
 RT "Complete genome sequence of the model actinomycete *Streptomyces*  
 RT *coelicolor* A3(2),"  
 RL Nature 417:141-147(2002).  
 DR EMBL; AL939117; CAC10303.1; -;  
 DR InterPro; IPR002550; CBS.  
 DR InterPro; IPR000844; CBS\_domain.

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DR InterPro; IPR005170; CorC_transpt-asc.
DR Pfam; PF00571; CBS; 2.
DR Pfam; PF03471; CorC_HlyC; 1.
DR Pfam; PF01595; DUF21; 1.
DR SMART; SM00116; CBS; 1.
DR Complete proteome.
KW SEQUENCE 459 AA; E96CE64003F45752 CRC64;

Query Match          15.0%; Score 75.5; DB 16; Length 459;
Best Local Similarity 31.5%; Pred. No. 72;
Matches 34; Conservative 12; Mismatches 49; Indels 13; Gaps 5;

QY 3 LAALLGLCVALSCTSSAAFLVGSAPVQVALESAAEAGAGTLANPLGTLNPKLLLS 62
DB 5 LLLLLALLLLTAC--ALFVAASFLLTVERSLLERAAESGERGADGALRAVRSITLQLS 61
QY 63 --SIGIPVNHLEIG--SOKCVAEI--GPQAV-----CAVKALKALIGAL 100
DB 62 GAQLGHTVTSLVGMIAEPSVILLRGLPTAMGLGGAATVATLLGV 109

RESULT 18
Q8G3S5 PRELIMINARY; PRT; 496 AA.
AC Q8G3S5;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE Hypothetical secreted protein with D-Ala-D-Ala carboxypeptidase 3
DE (S13) domain.
GN BL1679.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NC 2705.
RX MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karimantou M., Snel B., Villanova D., Berger B.,
RA Pessi G., Zwahlen M.-C., Desiere F., Bork P., Delley M.,
RA Fridmore R.D., Arigoni F.
RA "The genome sequence of Bifidobacterium longum reflects its adaptation
RA to the human gastrointestinal tract.";
RA Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AB014802; AA025466.1;
DR GO; GO:0004185; F:serine carboxypeptidase activity; IEA.
DR GO; GO:0006508; P:proteolysis and peptidolysis; IEA.
DR InterPro; IPR00667; Peptidase S13.
DR Pfam; PF02113; Peptidase S13; 1.
DR PRINTS; PR00922; DADACBP7ASE3.
DR TIGRFAMs; TIGR00666; PB24. 1.
KW Hypothetical protein; Carboxypeptidase; Complete proteome.
SQ SEQUENCE 496 AA; 50623 MW; 41572806ACD2D292 CRC64;

Query Match          15.0%; Score 75.5; DB 16; Length 496;
Best Local Similarity 30.3%; Pred. No. 78;
Matches 36; Conservative 15; Mismatches 43; Indels 25; Gaps 6;

QY 3 LAALLGLCVALSCTSSAAFLVGSAPVQVALESAAEAGAGTLANPLGTLNPKL--- 59
DB 36 IALFAGYCAADITVAPGLL--TLKPVTAPVFADPAKSG-GTVA---GTLNANKAIDS 89
QY 60 -----LLSLGI--PVNHLIEGSKQVA-----ELGFQVAGVAKKALLGALT 102
DB 90 TAASALVNNLLSAQGVGNDA5VIEDAQGTVAEHSNTPREPASTLTKLTALAASTL 148

RESULT 19
Q9VEG2 PRELIMINARY; PRT; 544 AA.
ID Q9VEG2
AC Q9VEG2;
DT 01-NOV-1999 (TrEMBLrel. 12, Created)
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DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Hypothetical protein AP50614.
GN AP50614.
OS Aeropyrum pernix.
OC Archaea; Crenarchaeota; Thermoprotei; Desulfurococcales;
OC Desulfurococceae; Aeropyrum.
OX NCBI_TaxID=56636;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=K1.
RX MEDLINE=99310339; PubMed=10382966;
RA Kawarabayashi Y., Hino Y., Horikawa H., Yamazaki S., Haikawa Y.,
RA Jin-to K., Takahashi M., Sekine M., Baba S.-I., Ankai A., Kosugi H.,
RA Hosoyama A., Fukui S., Nagai Y., Nishijima K., Nakazawa H.,
RA Takamiya M., Masuda S., Funahashi T., Tanaka T., Kudoh Y.,
RA Yamazaki J., Kishida N., Oguchi A., Aoki K.-I., Kubota K.,
RA Nakamura Y., Nomura N., Sako Y., Kikuchi H.
RA "Complete genome sequence of an aerobic hyper-thermophilic
RA crenarchaeon, Aeropyrum pernix K1.";
RT DNA Res. 6:83-101(1999).
RL EMBL; AP000060; BAA79584.1;
DR PIR; H72647; H72647.
DR GO; GO:0005215; F:transporter activity; IEA.
DR GO; GO:0006810; P:transport; IEA.
DR InterPro; IPR00566; Lipocln_cytFABP.
DR PROSITE; PS00213; LIPOCALIN_1.
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 544 AA; 55839 MW; 14028D4D558A7891 CRC64;

Query Match          15.0%; Score 75.5; DB 17; Length 544;
Best Local Similarity 26.4%; Pred. No. 86;
Matches 33; Conservative 19; Mismatches 36; Indels 37; Gaps 5;

QY 5 ALLGLCVALSCTSSA-----AFLVGSAPVQVA-----LESAAEAGAGTLANP 50
DB 18 ALVAVAVAVAAALMSVGGRTAGLAGAAASOSIAAASNPFLYMEAWVEAGA----- 71
QY 51 LGTLNPKLLLSLGI--PVNHLI-----EGSQKVAELGPQAVGAVKALK-----ALIGA 99
DB 72 -----LKVRFYSPGAPVSVVLPKPGEGVAARVELPEPVGVDMEGVDCSPVLGV 125
QY 100 LTVFG 104
DB 126 ETVGG 130

RESULT 20
Q8XRMS PRELIMINARY; PRT; 667 AA.
ID Q8XRMS
AC Q8XRMS;
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE Probable signal peptide protein.
GN RSP083 OR RS01904.
OS Ralstonia solanacearum (Pseudomonas solanacearum).
OG Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Burkholderiaceae; Ralstonia.
OX NCBI_TaxID=305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=GMI1000;
RX MEDLINE=21681879; PubMed=11823852;
RA Salanoubat M., Genin S., Artiguenave F., Gouzy J., Mangenot S.,
RA Arlat M., Billault A., Brottier P., Camus J.-C., Cattoir L.,
RA Chandler M., Choisein N., Claudel-Renard C., Cunnac S., Denange N.,
RA Gaspin C., Lavie M., Moisan A., Robert C., Saurin W., Schiex T.,
RA Siguer P., Thebaud P., Whalen M., Wincker P., Levy M.,
RA Weissenbach J., Boucher C.A.;
RT "Genome sequence of the plant pathogen Ralstonia solanacearum.";
RL Nature 415:497-502(2002).
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DR EMBL; AL646081; CAD17954.1; -;  
DR GO; GO:0046821; C:extrachromosomal DNA; IEA.  
KW Plasmid; Complete proteome.  
SQ SEQUENCE 667 AA; 59635 MW; 7C78268AC33B9E2B CRC64;  
  
Query Match 15.0%; Score 75.5; DB 16; Length 667;  
Best Local Similarity 29.1%; Pred. No. 1.1e+02;  
Matches 30; Conservative 14; Mismatches 44; Indels 15; Gaps 3;  
  
QY 14 SCSSAAAFVGSAXVQVAPVAALSAEABAGA-----GTLANPLGTNPLKLL---LSSLG 65  
Db 498 SVGSGGALAPVQGVYVQVGTGLGNSPTGALSGVGVGTGAGSNPAGALTGSLGIG 557  
  
QY 66 IPVNH-----IEGSKQVAEIQPQVAGVAKKALLGALT 101  
Db 558 APVSQVGSLSLTPVGGSGVGVQVGGVAGVAGGSLGVS 600  
  
RESULT 21  
Q89XU3 PRELIMINARY; PRT; 299 AA.  
AC Q89XU3;  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE BL0213 protein.  
GN BL0213.  
OS Bradyrhizobium japonicum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Bradyrhizobium.  
OX NCBI\_TaxID=375;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USDA 110;  
RX MEDLINE=22484998; PubMed=12597275;  
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
SA Samoto S., Watanabe A., Ideasa K., Iriguchi M., Kawashima K.,  
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,  
RA Tabata S.;  
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
Bradyrhizobium japonicum USDA110."  
RL DNA Res. 9:189-197(2002).  
DR EMBL; AP005935; BAC45478.1; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR InterPro; IPR000620; DUF6.  
DR Pfam; PF00892; DUF6; 1.  
KW Complete proteome.  
SQ SEQUENCE 299 AA; 31937 MW; 86F2F929C7B18E94 CRC64;  
  
Query Match 14.9%; Score 75; DB 16; Length 299;  
Best Local Similarity 25.5%; Pred. No. 50;  
Matches 25; Conservative 22; Mismatches 47; Indels 4; Gaps 1;  
  
QY 3 LAALLGLCVALSAAAFVGSAXVQVAPVAALSAEABAGAAGTLANPLGTNPLKLLS 62  
Db 81 LSGIVGTGLMLLAMDNRSPVVTAYLKTETAI---QTAIFGVELGDHLTLKLVLAIVA 136  
  
QY 63 SGIGPWNHIEGSKQVAEIQPQVAGVAKKALLGAL 100  
Db 137 TIGVITALRPGGEKSFALKEKTLILGVAAAFALSAV 174  
  
RESULT 22  
Q8RPK5 PRELIMINARY; PRT; 355 AA.  
AC Q8RPK5;  
DT 01-JUN-2002 (TReMBLrel. 21, Created)  
DT 01-JUN-2002 (TReMBLrel. 21, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE FGA.  
GN FGA.  
OS Corynebacterium pseudotuberculosis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxID=1719;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=Whetten 1;  
RX MEDLINE=21932508; PubMed=11934492;  
RA Billington S.J., Emay P.A., Songer J.G., Joist B.H.;  
RT "Identification and role in virulence of putative iron acquisition  
genes from Corynebacterium pseudotuberculosis.";  
RL FEMS Microbiol. Lett. 208:41-45(2002).  
DR EMBL; AP401634; AAL79811.1; -;  
DR GO; GO:0006020; C:membrane; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR000522; FecD.  
DR Pfam; PF01032; FecD; 1.  
SQ SEQUENCE 355 AA; 36205 MW; F4DCF004C98FCBB CRC64;  
  
Query Match 14.9%; Score 75; DB 2; Length 355;  
Best Local Similarity 28.2%; Pred. No. 61;  
Matches 29; Conservative 24; Mismatches 32; Indels 18; Gaps 5;  
  
QY 12 ALSGSSAAAF-----LVGSAKEVQVAPVAALSAEABAGAAGTLANPLG-----TLNPLKL 59  
Db 116 ALGINSGAFVAVVGVIALFGASSPWFALALLGA--CGAAAVVSVGTHRSATADPVL 173  
  
QY 60 LLSLGIPTVNHIEGSKQVAEIQPQVAGVAKKALLGALT 102  
Db 174 VLS--GVALSAILSGIGELSLVNPQAFDLKSW--MVGSDV 212  
  
RESULT 23  
Q89H46 PRELIMINARY; PRT; 370 AA.  
AC Q89H46;  
DT 01-JUN-2003 (TReMBLrel. 24, Created)  
DT 01-JUN-2003 (TReMBLrel. 24, Last sequence update)  
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)  
DE ABC transporter permease protein.  
GN BLR6149.  
OS Bradyrhizobium japonicum.  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Bradyrhizobiaceae; Bradyrhizobium.  
OX NCBI\_TaxID=375;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=USDA 110;  
RX MEDLINE=22484998; PubMed=12597275;  
RA Kaneko T., Nakamura Y., Sato S., Minamisawa K., Uchiumi T.,  
SA Samoto S., Watanabe A., Ideasa K., Iriguchi M., Kawashima K.,  
RA Kohara M., Matsumoto M., Shimpo S., Tsuruoka H., Wada T., Yamada M.,  
RA Tabata S.;  
RT "Complete genomic sequence of nitrogen-fixing symbiotic bacterium  
Bradyrhizobium japonicum USDA110."  
RL DNA Res. 9:189-197(2002).  
DR EMBL; AP005957; BAC51414.1; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005215; F:transporter activity; IEA.  
DR InterPro; IPR001851; Bac\_inmem\_transp.  
DR Pfam; PF02653; BPD\_transp\_2; 1.  
KW Complete proteome.  
SQ SEQUENCE 370 AA; 613481F38466F22A CRC64;  
  
Query Match 14.9%; Score 75; DB 16; Length 370;  
Best Local Similarity 28.2%; Pred. No. 63;  
Matches 33; Conservative 17; Mismatches 45; Indels 22; Gaps 5;  
  
QY 3 LAALLGLCV-----ALSCSSAAAFVGSAXVQVAPVAALSAEABAGA-----AGTL 47  
Db 96 LPAQLGMVIGGEGALLGALSATSAALQGMPLPVQIAMVIAGVIGGLMIMLSGAL 155  
  
QY 48 ANPLG---TLNPLKLLSSIGIPVNHIEGSKQVAEI---GPOAVGAVKALKALIG 98

156 ROYGVNETISLLVYIALAI-LNELVEGLMRDPASLNKPKSTREIGRANMIGSIPG 211

Db Q8C313 PRELIMINARY; PRT; 463 AA.

AC Q8C313; 23, Created)

DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)

DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE SNF1-like kinase (Fragment).

OS Mus musculus (Mouse).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

OX NCBI\_TaxID=10090;

EN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=CS7BL/6J; TISSUE=Lung;

RX MEDLINE=22354683; PubMed=12466851;

RA THE FANTOM Consortium,

RA the RIKEN Genome Exploration Research Group Phase I & II Team;

RT "Analysis of the mouse transcriptome based on functional annotation of

RT 60,770 full-length cDNAs."

RL Nature 420:563-573(2002).

DR EMBL; AK087322; BAC39845.1; -.

FT NON-TER

SQ SEQUENCE 463 AA; 48366 MW; DA6327DB4AF27C78 CRC64;

Query Match 14.9%; Score 75; DB 11; Length 463;

Best Local Similarity 34.2%; Pred. No. 81;

Matches 27; Conservative 10; Mismatches 30; Indels 12; Gaps 3;

QY 10 CVALSCSAAAFVLSAKPVAQVVALESAAEAGAGTLANP--LGTLPNPKLLLSLIGP 67

Db 174 CVIVSSSATAPSGTSDSCLPFSAGEAGLGSG-LATPGLLTSSPVLASPLF--- 229

QY 68 VNHLEGSQKCVBELGPOA 86

Db 230 -----GSQATPVLQTA 242

RESULT 25

Q9LOK1

ID Q9LOK1 PRELIMINARY; PRT; 611 AA.

AC Q9LOK1;

DT 01-OCT-2000 (TREMBLrel. 15, Created)

DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Putative membrane protein.

GN SCO4654 OR SCD40A.10C.

OS Streptomyces coelicolor.

OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;

OC Streptomycineae; Streptomycetaceae; Streptomyces.

OX NCBI\_TaxID=1902;

EN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RA Seeger K.J., Harris D.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

EN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RA Cerdeno A.M., Parkhill J., Barrell B.G., Rajandream M.A.;

RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

EN [3]

RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);

RA Redenbach M., Kiese H.M., Denapalte D., Eichner A., Cullum J.,

RA Kinashi H., Hopwood D.A.;

RT "A set of ordered cosmid and a detailed genetic and physical map for

RT the 8 Mb Streptomyces coelicolor A3(2) chromosome."

Mol. Microbiol. 21:77-96 (1996).

[4]

RL SEQUENCE FROM N.A.

RP STRAIN=A3(2) / M145;

RX MEDLINE=2196410; PubMed=12000953;

RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,

RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kiese H.,

RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,

RA Cronin A., Fraser A., Godle A., Hidalgo J., Hornsby T., Howarth S.,

RA Huang C.-H., Kiese T., Larke L., Murphy L., Oliver K., O'Neill S.,

RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,

RA Seeger K., Saunders D., Sharp S., Squares S., Taylor K.,

RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,

RA Hopwood D.A.;

RT "Complete genome sequence of the model actinomycete Streptomyces

RT coelicolor A3(2).";

RL Nature 417:141-147(2002).

DR EMBL; AL939121; CAB81855.1; -.

DR GO; GO:0016020; C:membrane; IEA.

DR InterPro; IPR003838; DUF214.

DR Pfam; PF02687; FtsX; 2.

KW Complete proteome.

SQ SEQUENCE 611 AA; 61744 MW; 8F959720773AEDF9 CRC64;

Query Match 14.7%; Score 74; DB 16; Length 611;

Best Local Similarity 41.9%; Pred. No. 1.3e+02;

Matches 26; Conservative 9; Mismatches 21; Indels 6; Gaps 2;

QY 3 LAALIGLVALSCSAAAFVLSAKPVAQVVALESAAEAGAGTLANPGLTLPNPKLLIS 62

Db 134 LAFWTGLLVALCGAAASWAGRTGPVE---ALREAAADAGATTGR---WLSGLALLJT 187

QY 63 SL 64

Db 188 AL 189

RESULT 26

Q86D11

ID Q86D11 PRELIMINARY; PRT; 119 AA.

AC Q86D11;

DT 01-JUN-2003 (TREMBLrel. 24, Created)

DT 01-JUN-2003 (TREMBLrel. 24, Last sequence update)

DT 01-JUN-2003 (TREMBLrel. 24, Last annotation update)

DE Stage-specific S antigen-like protein.

OS Leishmania infantum.

OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.

OX NCBI\_TaxID=5671;

EN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=MHOM/FR/92/LEM385;

RA Garin Y.J.-F., Meneceur P., Lorenzo F., Bui H., Pratlong F.,

RA Blanche H., Dedet J.-P., Derouin F.;

RL Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY255809; AAP21105.1; -.

SQ SEQUENCE 119 AA; 11523 MW; E32E2EC612D720EC CRC64;

Query Match 14.6%; Score 73.5; DB 5; Length 119;

Best Local Similarity 28.8%; Pred. No. 26;

Matches 30; Conservative 16; Mismatches 33; Indels 25; Gaps 4;

QY 1 MKLAALIGLVALSCSAAAFVLSAKPVAQVVALESAAEAGAGTLANPGLTLPNPKLL 60

Db 1 MKIRSVRPLVLLVCVAAVLALSAEPP-----HKAAYDAG-----PLSVD 41

QY 61 LSSIGIPVNHLEGSQKVAELGPOAVG--AVKALKALLGALT 102

Db 42 VGPLSVGVPLSVGPQ-----SVGPLSVGPOSVDPLSVGVPLSV 81

RESULT 27

Q9HNI9

ID Q9HNI9 PRELIMINARY; PRT; 331 AA.

AC Q9HNI9;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)  
DT 01-MAR-2001 (TrEMBLrel. 16, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Transport protein.  
GN PHNE OR VNG2084G.  
OS Halobacterium sp. (strain NRC-1 / ATCC 700922 / JCM 11081).  
OC Archaea; Euryarchaeota; Halobacteria; Halobacteriales;  
OC Halobacteriaceae; Halobacterium.  
OX NCBI\_TaxID=64091;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=20504483; PubMed=11016950;  
RA Ng W.V., Kennedy S.P., Mahairas G.G., Berquist B., Pan M.,  
RA Shukla H.D., Laasy S.R., Baliga N.S., Thorsson V., Sirogna J.,  
RA Swartzell S., Weir D., Hall J., Dahl T.A., Welte R., Goo Y.A.,  
RA Leithauer B., Keller K., Cruz R., Danson M.J., Hough D.W.,  
RA Maddocks D.G., Jablonski P.E., Krebs M.P., Angevine C.M., Dale H.,  
RA Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,  
RA Alam M., Freitas T., Hou S., Daniels C.J., Dennis P.P., Omer A.D.,  
RA Ebhardt H., Lowe T.M., Liang P., Riley M., Hood L., Dassarma S.,  
RT "Genomic sequence of Halobacterium species NRC-1";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:12176-12181(2000).  
DR EMBL; AB005098; AG20231.1; -;  
DR F01; C84358; C84358.  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005524; P:ATP binding; IEA.  
DR GO; GO:0005215; P:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR000515; BPT\_transp.  
DR InterPro; IPR005479; CPase\_L\_D2.  
DR Pfam; PF0528; BPT\_transp; 1.  
DR PROSITE; PS00867; CFSASE\_2; 1.  
KW Complete proteome.  
SQ SEQUENCE 331 AA; 36613 MW; 5AC660A5C6EA0E44 CRC64;  
  
Query Match 14.6%; Score 73.5; DB 17; Length 331;  
Best Local Similarity 27.9%; Pred. No. 77;  
Matches 29; Conservative 17; Mismatches 35; Indels 23; Gaps 5;  
  
QY 3 LAALGLCVALSCTSSAAAFVGSAPQVPAALSAEAGAGTANPLGTLPKLLS 62  
Db 83 LTLGVPVFDVGVGYFLAAHNP-SIPLAAVETLGIAPAGV---LGA-PLALTFG 136  
  
QY 63 SLG-----IPVNHIEGSKQVAGLGPQVAVKALKALIGAL 100  
Db 137 VLGSERVTFPLNPLFRG-----VMSIRSIPALVWAL 169  
  
RESULT 28  
Q8NQ28 PRELIMINARY; PRT; 358 AA.  
AC Q8NQ28;  
DT 01-OCT-2002 (TrEMBLrel. 22, Created)  
DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE ABC-type transporter, permease components.  
GN CGL1626.  
OS Corynebacterium glutamicum (Brevibacterium flavum).  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Corynebacterineae; Corynebacteriaceae; Corynebacterium.  
OX NCBI\_TaxID=1718;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=ATCC 13032 / DSM 20300 / NCIB 10025;  
RA Nakagawa S.;  
RT "Complete genomic sequence of Corynebacterium glutamicum ATCC 13032.";  
RL Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AF005279; BAB99019.1; -;  
DR GO; GO:0016020; C:membrane; IEA.  
DR GO; GO:0005215; P:transporter activity; IEA.  
DR GO; GO:0006810; P:transport; IEA.  
DR InterPro; IPR001651; Bac\_inmem\_transp.

DR InterPro; IPR000522; FecD.  
DR Pfam; PF01032; FecCD; 1.  
DR ProDom; PD001557; FecCD; 1.  
KW Complete proteome.  
SQ SEQUENCE 358 AA; 37275 MW; 7F3AA9BF28BE2607 CRC64;  
  
Query Match 14.6%; Score 73.5; DB 16; Length 358;  
Best Local Similarity 26.5%; Pred. No. 84;  
Matches 27; Conservative 19; Mismatches 45; Indels 11; Gaps 3;  
  
QY 6 LLGLCVALSCTSSAAAFVGSAPQVPAALSAEAGAGT-----LANPLGTLPK 58  
Db 115 TLGVNSGASCGAAALLFGVGAGFGD--YALQSAFLGMAASGLIFFVARAAGRISSTR 172  
  
QY 59 LLLSLGIPVNHIEGSKQVAGLGPQVAVKALKALIGAL 100  
Db 173 LLMS--GAIGYMLSAATSFLLSSDSAGSRSVFLWLLGSL 212  
  
RESULT 29  
Q8EJ01 PRELIMINARY; PRT; 389 AA.  
AC Q8EJ01;  
DT 01-MAR-2003 (TrEMBLrel. 23, Created)  
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)  
DT 01-OCT-2003 (TrEMBLrel. 25, Last annotation update)  
DE Prophage MuSol, protein Gp32, putative.  
GN SO0674  
OS Shewanella oneidensis.  
OC Bacteria; Proteobacteria; Gammaproteobacteria; Alteromonadales;  
OC Alteromonadaceae; Shewanella.  
OX NCBI\_TaxID=70863;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MR-1;  
RX MEDLINE=22297686; PubMed=12368813;  
RA Heidelberg J.F., Paulsen I.T., Nelson K.E., Gaidos E.J., Nelson W.C.,  
RA Read T.D., Eisen J.A., Seshadri R., Ward N., Methe B., Clayton R.A.,  
RA Meyer T., Tsapin A., Scott J., Bearan M., Brinkac L., Daugherty S.,  
RA DeBoy R.T., Dodson R.J., Durkin A.S., Haft D.H., Kolonay J.F.,  
RA Madupu R., Peterson J.D., Umayam L.A., White O., Wolf A.M.,  
RA Vamathavan J., Weidman J., Imprim M., Lee K., Berry K., Lee C.,  
RA Vueller J., Khouri H., Gill J., Utterback T.R., McDonald L.A.,  
RA Feldblyum T.V., Smith H.O., Venter J.C., Nealon K.H., Fraser C.M.;  
RT "Genome sequence of the dissimilatory metal ion-reducing bacterium Shewanella oneidensis.";  
RL Nat. Biotechnol. 20:1118-1123(2002).  
DR EMBL; AE015513; AAN53752.1; -;  
DR TIGR; SO0674; -;  
DR GO; GO:0019028; C:viral capsid; IEA.  
DR GO; GO:0005198; F:structural molecule activity; IEA.  
DR InterPro; IPR001337; TMV\_coat.  
KW Complete proteome.  
SQ SEQUENCE 389 AA; 41160 MW; 4241380685706AEB CRC64;  
  
Query Match 14.6%; Score 73.5; DB 16; Length 389;  
Best Local Similarity 33.0%; Pred. No. 92;  
Matches 29; Conservative 12; Mismatches 26; Indels 21; Gaps 4;  
  
QY 32 FVAALSAEAGAGTANPLG-----TLNPKL-LLSLGIPIVNHIEGSKQVAGL 82  
Db 173 PLALALAAALDTSLNALPHPTQPEGLHVNPPLMKLLAALGI---ETAESEPTAQL 229  
  
QY 83 GP-----QAVGAVKALKALIGALT 101  
Db 230 NDALKRIDDLVKAAGSVGLKQEVAAUT 257.  
  
RESULT 30  
Q9GUB5 PRELIMINARY; PRT; 1468 AA.  
AC Q9GUB5;  
DT 01-MAR-2001 (TrEMBLrel. 16, Created)

DB 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)  
DE Heavy-chain fibroin (Fragment).  
GN FIB-H.  
OS Galleria mellonella (Wax moth).  
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pelegrina; Pyraloidea;  
OC Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia; Pyraloidea;  
OC Pyralidae; Galleriinae; Galleria.  
OX NCBI\_TaxID=7137;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=Posterior silk gland;  
RA Zurovec M., Kodrik D., Yang C., Sehna F.;  
RL "Heavy-chain fibroin of Galleria mellonella L.";  
DR Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.  
EMBL: AF095239; AAC10393.1;  
FT NON TER 1468 1468  
SQ SEQUENCE 1468 AA; 122705 MW; 2DA59E1181BB3DDF CRC64;  
Query Match 14.6%; Score 73.5; DB 5; Length 1468;  
Best Local Similarity 32.8%; Pred. No. 3.9e+02;  
Matches 29; Conservative 13; Mismatches 24; Indels 23; Gaps 4;  
QY 16 SAAAFVLSAKFVAQVPALE-----SAAEAGAGTIANPLGTINPLKLLSLGIPVNH 71  
DB 1234 SAAASAGAGFA--PVIVIEGSSAASAAAAGSGAGVGGLG-----LSALG----- 1280  
QY 72 IEGSQKQVAGLQVAVKALCAL 100  
DB 1281 -----PLGGIGPHGVSSASALGAGLGGV 1303  
RESULT 31  
Q98D48 PRELIMINARY; PRT; 317 AA.  
AC Q98D48;  
DT 01-OCT-2001 (TREMBlrel. 18, Created)  
DT 01-OCT-2001 (TREMBlrel. 18, Last sequence update)  
DE Hypothetical protein mll4860.  
GN Mll4860.  
OS Rhizobium loti (Mesorhizobium loti).  
OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;  
OC Phyllobacteriaceae; Mesorhizobium.  
OX NCBI\_TaxID=381;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=MAFF303059;  
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,  
RA Watanabe A., Idegawa K., Ishikawa A., Kawashima K., Kimura T.,  
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,  
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto M.,  
RA Takeuchi C., Yamada M., Tabata S.;  
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium  
RT Mesorhizobium loti";  
RL DNA Res. 7:331-338(2000).  
DR EMBL: AP003005; BAB51423.1; -;  
DR GO: GO:0016020; C:membrane; IEA.  
DR GO: GO:0008324; F:cation transporter activity; IEA.  
DR GO: GO:0006812; P:cation transport; IEA.  
DR InterPro: IPR002524; C:cation efflux.  
DR Pfam: PF01545; C:cation efflux; 1.  
DR TIGRFAMs: TIGR01297; CDP; 1.  
KW Hypothetical protein; Complete proteome.  
SQ SEQUENCE 317 AA; 34064 MW; 36E60C5E58C72A54 CRC64;  
Query Match 14.5%; Score 73; DB 16; Length 317;  
Best Local Similarity 31.1%; Pred. No. 82;  
Matches 38; Conservative 15; Mismatches 39; Indels 30; Gaps 7;  
QY 4 AALIG-LCVALSASSAAFLVGSAPVPALESAAEAGAGTL-----ANPLGTL 54  
DB 1234 AALIG-LCVALSASSAAFLVGSAPVPALESAAEAGAGTL-----ANPLGTL 54

DB 13 AALAGNLAIT-KFAAAPTGTSSAMLSGV---HSLVDITGNGGLLYGMHRAAPADRT 68  
QY 55 NPL-----KLLSSSLGIPVNHLEGSQKQVAGLQVAVKALCALCAL 101  
DB 69 HPLGHGRLYFWSFVALLVFGAGVS-LYEGIIHIA---PEPVANVKVYIVGLSLF 124  
QY 102 VF 103  
DB 125 LF 126  
RESULT 32  
Q825M1 PRELIMINARY; PRT; 429 AA.  
AC Q825M1;  
DT 01-JUN-2003 (TREMBlrel. 24, Created)  
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)  
DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
DE Putative ROK-family transcriptional regulator.  
GN SAV7436.  
OS Streptomyces avermitilis.  
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;  
OC Streptomyces; Streptomycetaceae; Streptomyces.  
OX NCBI\_TaxID=33903;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,  
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
RT "Genome sequence of an industrial microorganism Streptomyces  
RT avermitilis; deducing the ability of producing secondary  
RT metabolites";  
RL Proc. Natl. Acad. Sci. U.S.A. 98:12215-12220(2001).  
RN [2]  
RP SEQUENCE FROM N.A.  
RC STRAIN=NA-4680 / ATCC 31267 / NCIMB 12804 / NRRL 8165;  
RX MEDLINE=21477403; PubMed=11572948;  
RA Omura S., Ikeda H., Ishikawa J., Hanamoto A., Takahashi C.,  
RA Shinose M., Takahashi Y., Horikawa H., Nakazawa H., Osonoe T.,  
RA Kikuchi H., Shiba T., Sakaki Y., Hattori M.;  
RT "Complete genome sequence and comparative analysis of the industrial  
RT microorganism Streptomyces avermitilis";  
RL Nat. Biotechnol. 21:526-531(2003).  
DR EMBL: AP005050; BAC75147.1; -;  
DR InterPro: IPR006000; ROK.  
DR Pfam: PF00480; ROK; 1.  
DR Complete proteome.  
SQ SEQUENCE 429 AA; 45476 MW; DA40D29C898B4FDB CRC64;  
Query Match 14.5%; Score 73; DB 16; Length 429;  
Best Local Similarity 30.8%; Pred. No. 1.1e+02;  
Matches 32; Conservative 12; Mismatches 40; Indels 20; Gaps 4;  
QY 12 ALSGSSAAFLVGSAPVPALESAAE-AGAGTIANPLGTINPLKLL-----LS 62  
DB 295 ALTMLAAAVPGGADPDPAALAVLEETAAYLGAG-LSDLINLFQPERILIGWAGLQLG 353  
QY 63 SLGIP-----VNHLEGSQKQVAGLQVAVKALCAL 96  
DB 354 SRLFPAVRHATSVALRHPAERVSIDLGLGPDVATAGAILPL 397  
RESULT 33  
Q91512 PRELIMINARY; PRT; 502 AA.  
AC Q91512;  
DT 01-MAR-2001 (TREMBlrel. 16, Created)  
DT 01-MAR-2001 (TREMBlrel. 16, Last sequence update)  
DT 01-JUN-2003 (TREMBlrel. 24, Last annotation update)  
DE Probable aldehyde dehydrogenase.  
GN PA0747.  
OS Pseudomonas aeruginosa.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;  
 OC Pseudomonadaceae; Pseudomonas.  
 OX NCBI\_TaxID=287;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 15692 / PAOI;  
 RX MEDLINE=20437337; PubMed=10984043;  
 RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warriner P.,  
 RA Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.,  
 RA Garber R.L., Coltray L., Tolentino E., Westbrook-Wadman S., Yuan Y.,  
 RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,  
 RA Smith K.A., Spencer D.H., Wong K.K.-S., Wu Z., Paulsen I.T.,  
 RA Reizer J., Sailer M.H., Hancock R.E.W., Lory S., Olson M.V.,  
 RA "Complete genome sequence of Pseudomonas aeruginosa PAOI, an  
 RT opportunistic pathogen.";  
 RL Nature 406:959-964(2000).  
 DR EMBL; AB004509; AAG04136.1; --  
 DR PIR; F83553; F83553.  
 DR HSP; P56533; 1A4S.  
 DR GO; GO:0016491; P:oxidoreductase activity; IEA.  
 DR GO; GO:0008152; P:metabolism; IEA.  
 DR InterPro; IPR002086; Aldehyde\_dehydr.  
 DR Pfam; PF00171; aldedh; 1.  
 DR Complete proteome.  
 SQ SEQUENCE 502 AA; 54564 MW; 33B2ABDFDA3B4973 CRC64;  
 Query Match 14.5%; Score 73; DB 16; Length 502;  
 Best Local Similarity 29.1%; Pred. No. 1.3e+02;  
 Matches 32; Conservative 13; Mismatches 41; Indels 24; Gaps 5;  
 QY 4 AALLGLCVALSCTSSA-----AFLVGSK-----FVAQPVAALES-----AAGAGTL 47  
 Db 264 AQLVGLNVLGASCGAQRCAWISAFAVGAAREWIPPELAERMAVLPGHWDPPDAAYGPL 323  
 QY 48 ANPLGLTNLKLKLLSLGIPVNHLEGGKQVAE-----LGPQAVAV 90  
 Db 324 ISPAQRQVRVLIABGKAGAECLLDGSO-CQVEGYPNGVNLGTLTLPFAV 372  
 RESULT 34  
 Q8GYAL ID Q8GYAL PRELIMINARY; PRT; 542 AA.  
 AC Q8GYAL  
 DT 01-MAR-2003 (TREMBlrel. 23, Created)  
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Hypothetical protein (Atig04570).  
 GN Atig04570/tig11.17.  
 OS Arabidopsis thaliana (Mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;  
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; rosids;  
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.  
 OX NCBI\_TaxID=3702;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=cv, Columbia;  
 RA Seki M., Iida K., Satou M., Sakurai T., Akiyama K., Ishida J.,  
 RA Nakajima M., Enju A., Kamiya A., Narusaka M., Carninci P., Kawai J.,  
 RA Hayashizaki Y., Shinozaki K.;  
 RA "Arabidopsis thaliana full-length cDNA";  
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Cheuk R., Chen H., Kim C.-J., Shinn P., Bowser L., Carninci P.,  
 RA Chan M.M., Chang C.H., Dale J.M., Hayashizaki Y., Hsuan V.W.,  
 RA Ishida J., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B.,  
 RA Lee J.M., Lin J., Miranda M., Narusaka M., Nguyen M., Chodera C.S.,  
 RA Palm C.J., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,  
 RA Tang C.C., Tortum M., Wong C., Wu H.C., Yamada K., Yu G., Yuan S.,  
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;  
 RA "Arabidopsis ORF clones";  
 RT Submitted (MAR-2003) to the EMBL/GenBank/DBJ databases.  
 RL EMBL; AK117774; BAC42421.1; --

DR EMBL; BT005916; AA064851.1; --  
 DR GO; GO:0016020; C:membrane; IEA.  
 DR GO; GO:0004553; P:hydrolase activity, hydrolyzing O-glycosyl . . .; IEA.  
 DR GO; GO:0005975; P:carbohydrate metabolism; IEA.  
 DR InterPro; IPR004324; BTL.  
 DR InterPro; IPR001547; Glyco\_hydro\_5.  
 DR Pfam; PF03092; BTL1; 1.  
 DR TIGRFAMS; TIGR00788; fbt; 1.  
 DR PROSITE; PS00659; GLYCOSYL\_HYDROL\_F5; 1.  
 KW Hypothetical protein.  
 SQ SEQUENCE 542 AA; 59479 MW; 839B45F3FDD261B8 CRC64;  
 Query Match 14.5%; Score 73; DB 10; Length 542;  
 Best Local Similarity 28.2%; Pred. No. 1.5e+02;  
 Matches 35; Conservative 16; Mismatches 49; Indels 24; Gaps 4;  
 QY 3 LAALLGLCVALSCTSSAFAFLVGSAPVAPVAALESAAEA-GAGTLANPLGLTNPLKLL 61  
 Db 233 LGSLLGGYLLLTTPKISFLVFSALLSLQLVLSLSSKEESFGLPRIAEVSSVLESVKQI 292  
 QY 62 SSL-----GIPVNHLEGGKQK-----VAELGPQAVGAKAL-KALLG 98  
 Db 293 SNLKEAIQADEISQPLIWAIVSVIAMVLLSGSVFCYQTVNLNDPSVIGMSKVGQIMLL 352  
 QY 99 ALTV 102  
 Db 353 CLTV 356  
 RESULT 35  
 Q9AAR5 ID Q9AAR5 PRELIMINARY; PRT; 584 AA.  
 AC Q9AAR5  
 DT 01-JUN-2001 (TREMBlrel. 17, Created)  
 DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)  
 DT 01-OCT-2003 (TREMBlrel. 25, Last annotation update)  
 DE Gamma-glutamyltransferase.  
 GN CC0531  
 OS Caulobacter crescentus.  
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;  
 OC Caulobacteraceae; Caulobacter.  
 OX NCBI\_TaxID=155892;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=ATCC 19089 / CB15;  
 RX MEDLINE=21173698; PubMed=11259647;  
 RA Nierman W.C., Feldblyum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,  
 RA Eisen J., Heidelberg J.F., Alley M.R.K., Chit N., Maddock J.R., Ely B.,  
 RA Potocka I., Nelson W.C., Newton A., Stephens C., Phadke N.D., Haft D.H.,  
 RA DeBoy R.T., Dodson R.J., Durkin A.S., Gwinn M.B., Haft D.H.,  
 RA Kolonay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,  
 RA Uterback T., Tran K., Wolf A., Vamathevan J., Ermolaeva M., White O.,  
 RA Salzberg S.L., Venter J.C., Shapiro L., Fraser C.M.;  
 RA "Complete genome sequence of Caulobacter crescentus.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 98:4138-4141(2001).  
 DR EMBL; AB005725; AAK22518.1; --  
 DR PIR; B87315; B87315.  
 DR MEROPS; T03.001; --  
 DR TIGR; CC0531; --  
 DR GO; GO:0003840; P:gamma-glutamyltransferase activity; IEA.  
 DR GO; GO:0016740; P:transferase activity; IEA.  
 DR InterPro; IPR00101; Peptidase\_13.  
 DR Pfam; PF01019; G\_glu\_transsept; 1.  
 DR PRINTS; PR01210; GGTRANSPTASE.  
 DR TIGRFAMS; TIGR00066; g\_glu\_trans; 1.  
 DR Transferase; Complete proteome.  
 KW TRANSFERASE  
 SQ SEQUENCE 584 AA; 61016 MW; 5C3DA03B02261E75 CRC64;  
 Query Match 14.5%; Score 73; DB 16; Length 584;  
 Best Local Similarity 28.6%; Pred. No. 1.6e+02;  
 Matches 28; Conservative 10; Mismatches 38; Indels 22; Gaps 2;  
 QY 2 KLAALLGLCVALSCTSSAFAFLVGSAPVAPV--AALESAAEAAGATLANPLGLTNPLKL 59

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Db 7 RLASLLSALQSLAPVAALAES:PLAWTPRPAATTPAKGMVAANPLAVEAGLVRV 66
Qy 60 LLSSLGIPVNHLEGGOKCVAELGPOAVGAVKALKALL 97
Db 67 LRD-----GGSAVDAVAIAQAVL 84

RESULT 36
Q7WL37 PRELIMINARY; PRT; 620 AA.
AC Q7WL37;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 1-deoxy-D-xylulose 5-phosphate synthase.
GN DXS OR BPP2464.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=RB50 / ATCC BAA-588;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640442; CAE32409.1; -.
KW Complete proteome.
SQ SEQUENCE 620 AA; 66230 MW; 5D023E312C76D694 CRC64;

Query Match 14.5%; Score 73; DB 16; Length 620;
Best Local Similarity 31.1%; Pred. No. 1.7e+02;
Matches 28; Conservative 11; Mismatches 31; Indels 20; Gaps 3;

Qy 12 ALSCSSAAFLVGSAPVQAPVAALSAEAGAGTLANPLGTLNPKLLSSLGIPVNH 71
Db 548 ALVTVEAAIMGGAGS-----AVLETLAAG-----VTLPLVLQGLPDAFI 588

RESULT 37
Q7W700 PRELIMINARY; PRT; 620 AA.
AC Q7W700;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 1-deoxy-D-xylulose 5-phosphate synthase.
GN DXS OR BPP2464.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
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RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640430; CAE37759.1; -.
KW Complete proteome.
SQ SEQUENCE 620 AA; 66230 MW; 5D023E312C76D694 CRC64;

Query Match 14.5%; Score 73; DB 16; Length 620;
Best Local Similarity 31.1%; Pred. No. 1.7e+02;
Matches 28; Conservative 11; Mismatches 31; Indels 20; Gaps 3;

Qy 12 ALSCSSAAFLVGSAPVQAPVAALSAEAGAGTLANPLGTLNPKLLSSLGIPVNH 71
Db 548 ALVTVEAAIMGGAGS-----AVLETLAAG-----VTLPLVLQGLPDAFI 588

RESULT 38
Q7VW87 PRELIMINARY; PRT; 620 AA.
AC Q7VW87;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 1-deoxy-D-xylulose 5-phosphate synthase.
GN DXS OR BPP2738.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=520;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Tohama I / ATCC BAA-589 / NCTC 13251;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
RA Harris D.E., Holden M.T.G., Churcher C.M., Bentley S.D., Mungall K.L.,
RA Cerdano-Tarraga A.M., Temple L., James K., Harris B., Quail M.A.,
RA Achtman M., Atkin R., Baker S., Basham D., Bason N., Cherevach I.,
RA Chillingworth T., Collins M., Cronin A., Davis P., Doggett J.,
RA Feltwell T., Goble A., Hamlin N., Hauser H., Holroyd S., Jagels K.,
RA Leather S., Moulé S., Norbertczak H., O'Neill S., Ormond D., Price C.,
RA Rabinowitsch E., Rutter S., Sanders M., Saunders D., Seeger K.,
RA Sharp S., Simmonds M., Skelton J., Squares R., Squares S., Stevens K.,
RA Unwin L., Whitehead S., Barrell B.G., Maskell D.J.;
RT "Comparative analysis of the genome sequences of Bordetella pertussis,
RT Bordetella parapertussis and Bordetella bronchiseptica."
RL Nat. Genet. 35:32-40(2003).
DR EMBL; BX640419; CAE343071.1; -.
KW Complete proteome.
SQ SEQUENCE 620 AA; 66260 MW; 4B561873485082A4 CRC64;

Query Match 14.5%; Score 73; DB 16; Length 620;
Best Local Similarity 31.1%; Pred. No. 1.7e+02;
Matches 28; Conservative 11; Mismatches 31; Indels 20; Gaps 3;

Qy 12 ALSCSSAAFLVGSAPVQAPVAALSAEAGAGTLANPLGTLNPKLLSSLGIPVNH 71
Db 548 ALVTVEAAIMGGAGS-----AVLETLAAG-----VTLPLVLQGLPDAFI 588

RESULT 39
Q7W700 PRELIMINARY; PRT; 620 AA.
AC Q7W700;
DT 01-OCT-2003 (TReMBLrel. 25, Created)
DT 01-OCT-2003 (TReMBLrel. 25, Last sequence update)
DT 01-OCT-2003 (TReMBLrel. 25, Last annotation update)
DE 1-deoxy-D-xylulose 5-phosphate synthase.
GN DXS OR BPP2464.
OS Bordetella pertussis.
OC Bacteria; Proteobacteria; Betaproteobacteria; Burkholderiales;
OC Alcaligenaceae; Bordetella.
OX NCBI_TaxID=519;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=12822 / ATCC BAA-587;
RX MEDLINE=22827954; PubMed=12910271;
RA Parkhill J., Sebahia M., Preston A., Murphy L.D., Thomson N.,
```

Db 589 DHGQRAALLAGLGLDAAAGIERAIRARFGAL 618

RESULT 39

O46099 PRELIMINARY; PRT; 1279 AA.

AC O46099; (TREMELrel. 06, Created)

DT 01-JUN-1998 (TREMELrel. 12, Last sequence update)

DT 01-JUN-2003 (TREMELrel. 24, Last annotation update)

DE EG:8DB.2 protein.

GN EG:8DB.2 OR CG11409.

OS Drosophila melanogaster (fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;

OC Ephydroidea; Drosophilidae; Drosophila.

OX NCBI\_TaxID=7227;

RN [1]

RN SEQUENCE FROM N.A.

RP STRAIN=Berkeley;

RC MEDLINE=20196006; PubMed=10731132;

RA Adams M.D., Ceiniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Ananides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,

RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,

RA Ballew R.M., Basu A., Baxterdale J., Beyrataroglu L., Beasley E.M.,

RA Beeson K.I., Benos P.V., Serman B.P., Bhandari D., Bolshakov S.,

RA Berkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,

RA Berts K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

RA Chertys J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,

RA Fostler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Hostin N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,

RA Houtin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,

RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Markulov G., Milshina N.V., Mobarry C., Morris J., Mostrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K.A., Nusskern D.R., Pacle J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinart K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,

RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,

RA Spier E., Spradling A.C., Stapieton M., Strong R., Sun E.,

RA Swirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,

RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,

RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,

RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "The genome sequence of Drosophila melanogaster."

RL Science 287:2185-2195(2000).

RN [2]

RN SEQUENCE FROM N.A.

RP Papagiannakis G., Spanos L., Cox S., Siden-Kiamos I., Louis C.,

RT "Sequencing the distal X chromosome of Drosophila melanogaster."

RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.

RN [3]

RN SEQUENCE FROM N.A.

RP Benos P.,

RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.

DR EMBL; AE003420; AAF45604.1; -

DR EMBL; AL022018; CAA17685.2; -

DR PIR; T13613; T13613.

DR FlyBase; FBgn0024366; EG:8DB.2.

SQ SEQUENCE 1279 AA; 139070 MW; FA96DBBA48C5D5E9 CRC64;

Query Match 14.5%; Score 73; DB 5; Length 1279;

Best Local Similarity 31.6%; Pred. NO. 3.7e+02;

Matches 31; Conservative 12; Mismatches 29; Indels 26; Gaps 4;

QY 25 SAKPVAQPVAALESAA-----AEAGAGTLANPLGTINPLKLLLSLGLPVPN 69

DB 213 SANPAAPSAARFSSHYSAKNAQFLRKPSEGGGSLSS---TVKPVADILESGLIVSG 269

QY 70 HIEGSK-----CVAEELGPQ-AGVAKKALKALLGA 99

DB 270 GKSDSAHKRYALDDYYPAESAPQPSVAVADLRGLHGA 307

RESULT 40

Q84CV5 PRELIMINARY; PRT; 240 AA.

AC Q84CV5;

DT 01-JUN-2003 (TREMELrel. 24, Created)

DT 01-JUN-2003 (TREMELrel. 24, Last sequence update)

DT 01-OCT-2003 (TREMELrel. 25, Last annotation update)

DE Lipoprotein VacJ.

GN VACJ.

OS Gamma-proteobacterium Hot 75m4.

OG Plasmid pAK211.

OC Bacteria; environmental samples.

OX NCBI\_TaxID=77133;

RN [1]

RN SEQUENCE FROM N.A.

RP MEDLINE=22560162; PubMed=12673061;

RA Kniesch A., Waschkowitz T., Bowien S., Henne A., Daniel R.,

RT "Metagenomes of Complex Microbial Consortia Derived from Different

RT Soils as Sources for Novel Genes Confering Formation of Carbonyls

RT from Short-Chain Polyols on Escherichia coli."

RL J. Mol. Microbiol. Biotech. 5:46-56(2003).

DR EMBL; AF548450; AA091899.1; -

DR GO; GO:004821; C:extrachromosomal DNA; IEA.

DR InterPro; IPR000437; Prok\_lipoprot\_S.

DR InterPro; IPR007428; VACJ.

DR Pfam; PF04333; VACJ; 1.

DR PRINTS; PR01805; VACJLIPOPROT.

DR PROSITE; PS00013; PROKAR\_LIPOPROTEIN; 1.

KW Lipoprotein; Plasmid.

SQ SEQUENCE 240 AA; 25861 MW; F0C945D05D258E99 CRC64;

Query Match 14.4%; Score 72.5; DB 2; Length 240;

Best Local Similarity 27.8%; Pred. NO. 68;

Matches 35; Conservative 10; Mismatches 46; Indels 35; Gaps 4;

QY 7 LGLCVALSCTSSAAA-----ELVGSAPVAQPVAALESAA- 40

DB 5 LPLTALAASLAAGCTTTDPSLAQNDPFPSNRAINFNVDKVAQPAARFYRAAV 64

QY 41 -EAGAGTLANPLGTINPLKLLLSLGLIPVNHLEIG-SQKVAELGPQAVGAVKALKALLG 98

DB 65 PEPARQGVHLENLNAIPVL-----VNDVLOGEKEKAVNTTGRFMVNSTVGLAGLID 117

QY 99 ALTVEFG 104

DB 118 VATEFG 123

Search completed: April 5, 2004, 14:35:28

Job time : 43 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on: April 5, 2004, 14:29:29 ; Search time 21 Seconds  
(without alignments)  
476.377 Million cell updates/sec

Title: US-09-997-428-408

Perfect score: 502

Sequence: 1 NKLALLGLCVALSASSAAA.....QAVGAVKALKALGALTVFG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283366 seqs, 96191536 residues

Total number of hits satisfying chosen parameters: 283366

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

PIR 78:\*\*

1: pir1:\*\*

2: pir2:\*\*

3: pir3:\*\*

4: pir4:\*\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	81	16.1	496	2 T09931	probable phosphodi
2	79.5	15.8	1381	2 S60004	hypothetical prote
3	77.5	15.4	601	2 T35054	probable transport
4	77	15.3	335	2 T36304	probable anthranil
5	76	15.1	355	2 A29773	hypothetical prote
6	76	15.1	355	2 G98309	probable ABC trans
7	76	15.1	699	2 H87275	thio-disulfide int
8	76	15.1	732	2 T47269	copper-transportin
9	75.5	15.0	544	2 H72647	hypothetical prote
10	73.5	14.6	331	2 C94358	transport protein
11	73	14.5	502	2 F83553	probable aldehyde
12	73	14.5	584	2 B87315	gamma-glutamyltran
13	73	14.5	1279	2 T36113	hypothetical prote
14	72	14.3	236	2 A56010	anastigote-specifi
15	72	14.3	397	2 A52900	succinyl-CoA synth
16	72	14.3	397	2 F97675	hypothetical prote
17	72	14.3	528	2 D70968	L-serine dehydrata
18	71.5	14.2	462	2 B87634	ATP-dependent Clp
19	71.5	14.2	874	2 A30370	endopeptidase clp
20	71.5	14.2	887	2 F98216	probable MPS trans
21	71	14.1	440	2 C83368	heat shock protein
22	70.5	14.0	668	2 G85160	probable endopepti
23	70.5	14.0	831	2 D71409	hypothetical prote
24	70	13.9	431	2 C86178	zinc finger protei
25	70	13.9	452	2 T46147	probable multidrug
26	70	13.9	477	2 D82179	hypothetical prote
27	69.5	13.8	244	2 S75653	hypothetical prote
28	69.5	13.8	396	2 G75454	probable PPE prote
29	69.5	13.8	423	2 C70582	

30	69.5	13.8	455	2 AD0782	probable L-serine
31	69	13.7	170	2 AF3312	hypothetical prote
32	69	13.7	627	2 D75393	serine proteinase,
33	69	13.7	853	2 T36551	probable ATP-denen
34	69	13.7	3295	2 A20074	probable adhesin Y
35	68.5	13.6	277	2 F84356	hypothetical prote
36	68.5	13.6	335	2 A50575	ferric enterobacti
37	68.5	13.6	1724	2 T18343	P-glycoprotein - S
38	68	13.5	334	2 S16296	ferric enterobacti
39	68	13.5	334	2 A85558	ferric enterobacti
40	68	13.5	334	2 A90707	ferric enterobacti
41	68	13.5	560	2 F70719	hypothetical prote
42	67.5	13.4	387	2 C75312	branched-chain ami
43	67.5	13.4	1179	2 H82706	hypothetical prote
44	67.5	13.4	1206	2 B87247	probable conserved
45	67.5	13.4	2698	2 B96671	similar to transla
46	67	13.3	218	2 F82220	glyoxylase II fami
47	67	13.3	228	2 D75048	aspartate racemase
48	67	13.3	290	2 S72996	probable glycoprot
49	67	13.3	351	2 S72817	probable glycoprot
50	67	13.3	419	2 A83619	leucine-specific b
51	67	13.3	636	2 F72736	hypothetical prote
52	67	13.3	724	2 H87423	cation-transportin
53	67	13.3	760	2 A82225	hypothetical prote
54	67	13.3	840	2 B87467	conserved hypothet
55	66.5	13.2	106	2 F86565	C7483 hypothetical
56	66.5	13.2	106	2 C72057	conserved hypothet
57	66.5	13.2	146	2 F72709	hypothetical prote
58	66.5	13.2	180	2 J00149	zein protein - mai
59	66.5	13.2	243	2 T36837	hypothetical prote
60	66.5	13.2	341	2 I55623	thromboxane A2 rec
61	66.5	13.2	465	2 G02738	FREAC-4 - human
62	66.5	13.2	667	2 T23010	hypothetical prote
63	66.5	13.2	873	2 F53225	ecdysone-induced p
64	66.5	13.2	1510	2 T13634	probable minor tal
65	66	13.1	118	2 S45680	lipic transfer pro
66	66	13.1	310	2 A80312	lyser-family trans
67	66	13.1	330	2 E82063	thiamin ABC transp
68	66	13.1	337	2 E84133	hypothetical prote
69	66	13.1	638	2 S22490	acetolactate synth
70	66	13.1	1400	2 B70963	hypothetical prote
71	66	13.1	1467	2 A75584	conserved hypothet
72	65.5	13.0	264	2 D7504	hypothetical prote
73	65.5	13.0	289	2 S70547	ssPB protein - Sal
74	65.5	13.0	343	2 F86412	F28N24.25 protein
75	65.5	13.0	361	2 H87700	citrate synthase I
76	65.5	13.0	491	2 C70868	hypothetical prote
77	65.5	13.0	593	2 S70216	siPB protein Sal
78	65.5	13.0	593	2 A10850	pathogenicity isla
79	65.5	13.0	665	2 G97819	hypothetical prote
80	65.5	13.0	848	2 G87220	heat shock protein
81	65.5	13.0	861	2 D82814	ATP-dependent Clp
82	65	12.9	267	2 F87665	hypothetical prote
83	65	12.9	275	2 B72484	hypothetical prote
84	65	12.9	276	2 T05778	hypothetical prote
85	65	12.9	312	2 H83245	hypothetical prote
86	65	12.9	367	2 A33649	hypothetical prote
87	65	12.9	385	2 H70503	iron(III)-binding
88	65	12.9	461	2 A31237	probable PPE prote
89	65	12.9	693	2 JH0265	DNA recombinase (E
90	65	12.9	845	2 T17291	hypothetical prote
91	65	12.9	4377	2 A55575	ankyrin 3, long sp
92	64.5	12.8	184	1 A41351	membrane-bound cyt
93	64.5	12.8	320	2 F64384	hypothetical prote
94	64.5	12.8	346	2 C87397	iron compound ABC
95	64.5	12.8	385	2 C83174	hypothetical prote
96	64.5	12.8	411	2 F84135	multidrug-efflux t
97	64.5	12.8	480	2 T35214	hypothetical prote
98	64.5	12.8	482	2 J07332	endoglycosylcerami
99	64.5	12.8	529	2 C82487	conserved hypothet
100	64.5	12.8	784	2 A26601	elastin precursor

ALIGNMENTS

RESULT 1  
T09931  
probable phosphodiesterase I (EC 3.1.4.1) / nucleotide diphosphatase (EC 3.6.1.9) T16L4.  
C/Species: Arabidopsis thaliana (mouse-ear cress)  
C/Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 16-Aug-2002  
C/Accession: T09931  
R/Bevan, M.; Rose, M.; Hempel, S.; Entian, K.D.; Bancroft, I.; Mewes, H.W.; Mayer, K.F.X.  
submitted to the Protein Sequence Database, June 1999  
A/Reference number: Z16897  
A/Accession: T09931  
A/Molecule type: DNA  
A/Residues: 1-496 <BEV>  
A/Cross-references: EMBL:AL079344; GSPDB:GN00062; ATSP:T16L4.190  
A/Experimental source: cultivar Columbia; EAC clone T16L4  
C/Genetics:  
A/Map position: 4  
C/Keywords: coenzyme A; metalloprotein; phosphoric diester hydrolase  
Query Match 16.1%; Score 81; DB 2; Length 496;  
Best Local Similarity 41.3%; Pred. No. 5.2; Mismatches 14; Indels 6; Gaps 3;  
Matches 26; Conservative 14  
QY 6 LGLCVALSAAFLVGSAXVQVPAVVALESABAGA--GTLANPLGTLN-PLKILLS 62  
DB 57 LLYVTCIALSAASAFALFFSSQ---KPVLSLNIQSKSPAFDRSVARPLKLDKPVVLLIS 113  
QY 63 SLG 65  
DB 114 SDG 116  
RESULT 2  
S60004  
hypothetical protein - common roundworm retrotransposon R4 (fragment)  
C/Species: Ascaris lumbricoideis. (common roundworm)  
C/Date: 19-Mar-1997 #sequence\_revision 25-Apr-1997 #text\_change 21-Jul-2000  
C/Accession: S60004  
R/Burke, W.D.; Mueller, F.; Eickbush, T.H.  
Nucleic Acids Res 23, 4628-4634, 1995  
A/Title: R4, a non-LTR retrotransposon specific to the large subunit rRNA genes of nemat  
A/Reference number: S60004; MUID:96103592; PMID:8524653  
A/Accession: S60004  
A/Status: preliminary; nucleic acid sequence not shown; translation not shown  
A/Molecule type: DNA  
A/Residues: 1-1381 <BUR>  
A/Cross-references: EMBL:U29445; NID:g903660; PID:AAA97394.1; PID:g903661  
A/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1995  
C/Genetics:  
A/Genome: retrotransposon  
Query Match 15.8%; Score 79.5; DB 2; Length 1381;  
Best Local Similarity 27.8%; Pred. No. 20;  
Matches 25; Conservative 15; Mismatches 23; Indels 27; Gaps 3;  
QY 11 VALSCSSAAFLVGSAXVQVPAVVALESAAAGAGT-----LANPLG----- 52  
DB 27 IAMPCTSTNFFERTGPBPHREFISGTSSLSLNGTHRSPLNDDEVINGPKGHESDPVH 86  
QY 53 -----TLNPLKLLSSLGIPVNHLEGSQ 76  
DB 87 VVRAPRTLHPRRL---ELPIGVNVLGEASQ 113  
RESULT 3  
T35054  
probable transport system permease protein - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 05-Nov-1999 #sequence\_revision 05-Nov-1999 #text\_change 05-Nov-1999

C/Accession: T35054  
R/Seeger, K.J.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, August 1998  
A/Reference number: Z21566  
A/Accession: T35054  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-601 <SEE>  
A/Cross-references: EMBL:AL031371; PIDN:CAA20556.1; GSPDB:GN00070; SCOEDB:SC4G2.19  
A/Experimental source: strain A3(2)  
C/Genetics:  
A/Gene: SCOEDB:SC4G2.19  
Query Match 15.4%; Score 77.5; DB 2; Length 601;  
Best Local Similarity 30.7%; Pred. No. 13;  
Matches 42; Conservative 10; Mismatches 48; Indels 37; Gaps 4;  
QY 3 LAALLGLCVALSAAAFVLSA--KPVA-----QPVAALESAAEAGAG----- 45  
DB 426 LVALLTVAGSGAATPALAVGAWAPLAHTSLLQERATLHITATKLGAGP VHLL 485  
QY 46 -----TLANPLGTLNPLKLLSSLG-----PVNHLEGSOKCVAEELGPQ 85  
DB 486 RHELLPAVVPVRLHALLRLPGVALASLGLGLGAQPPSPFWGLLAENQPYAERAPW 545  
QY 86 AYCAVKALKALIGALTV 102  
DB 546 AVLAAPAAVLALIGALAV 562  
RESULT 4  
T36304  
probable anthranilate phosphoribotransferase - Streptomyces coelicolor  
C/Species: Streptomyces coelicolor  
C/Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Jan-2000  
C/Accession: T36304  
R/Saunders, D.; Harris, D.; Bentley, S.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.  
submitted to the EMBL Data Library, March 1999  
A/Reference number: Z21604  
A/Accession: T36304  
A/Status: preliminary; translated from GB/EMBL/DBJ  
A/Molecule type: DNA  
A/Residues: 1-335 <SAU>  
A/Cross-references: EMBL:AL035654; PIDN:CAB38583.1; GSPDB:GN00070; SCOEDB:SCE8.05C  
A/Experimental source: strain A3(2)  
C/Genetics:  
A/Gene: trpD2; SCOEDB:SCE8.05C  
C/Superfamily: anthranilate phosphoribosyltransferase; trpD homology  
Query Match 15.3%; Score 77; DB 2; Length 335;  
Best Local Similarity 34.5%; Pred. No. 8.2;  
Matches 30; Conservative 9; Mismatches 36; Indels 12; Gaps 4;  
QY 7 LGLCVALSAAAFVLSA-----KPVAAQVVALESAA-----EAGAGTLANPLGTL-NP 56  
DB 117 LGVRIDLGAEAAACLDRTGITFLFAPVHP--APRHTAGPRRELGAFTVNLGLPLCNP 174  
QY 57 LKLLSSLGIPVNHLEGSOKCVAEELG 83  
DB 175 SGARLRTLGVPSELVEPMTVLERLG 201  
RESULT 5  
AD2973  
hypothetical protein Atu3389 [imported] - Agrobacterium tumefaciens (strain C58, Dupont  
C/Species: Agrobacterium tumefaciens  
C/Date: 11-Jan-2002 #sequence\_revision 11-Jan-2002 #text\_change 18-Nov-2002  
C/Accession: AD2973  
R/Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo,  
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutayavin, T.; Levy, R.; Li, M.; McCl1e1  
; Karp, P.; Romero, P.; Zhang, S.  
Science 294, 2317-2323, 2001  
A/Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,

ster, E.W.  
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.  
A:Reference number: AB2577; UID:21608550; PMID:11743193  
A:Accession: AD2973  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-355 <KUR>  
A:Cross-references: GB:AE008689; PIDN:AA44202.1; PID:g17741781; GSPDB:GN00187  
A:Experimental source: strain C58 (Dupont)  
C:Genetics:  
A:Gene: Atu3389  
A:Map position: linear chromosome

Query Match 15.1%; Score 76; DB 2; Length 355;  
Best Local Similarity 23.3%; Pred. No. 11;  
Matches 28; Conservative 22; Mismatches 42; Indels 28; Gaps 3;

QY 2 KLAALLGLCVALSAAFLVGSAPVAPVALESAAEAGAGTLANPLGTNPLKLL 61  
DB 24 RILILVGLFLALCFMSAADMALGPARYTLSEVLA-----TIADPAAVGNQLRVVI 73

QY 62 SSLGIPVNHLEGS-----IEGSKCVA-----ELGPQAVGAVKALKALGALTVF 103  
DB 74 WDIRPIALMAVTGASLSVAGAQNTILSNPLASPTFLGISAAASFGAALALVGGVAIF 133

RESULT 5  
G98309  
probable ABC transporter permease protein MJ0087 AGR\_L\_2865 [imported] - Agrobacterium tumefaciens  
C:Species: Agrobacterium tumefaciens  
C:Date: 22-Oct-2001 #sequence\_revision 22-Oct-2001 #text\_change 18-Nov-2002  
C:Accession: G98309  
R:Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldman, A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B.; Science 294, 2323-2328, 2001  
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tumefaciens  
A:Reference number: A97359; UID:21608551; PMID:11743194  
A:Accession: G98309  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-355 <KUR>  
A:Cross-references: GB:AE007870; PIDN:AAK90001.1; PID:g15159970; GSPDB:GN00170  
C:Genetics:  
A:Gene: AGR\_L\_2865  
A:Map position: linear chromosome

Query Match 15.1%; Score 76; DB 2; Length 355;  
Best Local Similarity 23.3%; Pred. No. 11;  
Matches 28; Conservative 22; Mismatches 42; Indels 28; Gaps 3;

QY 2 KLAALLGLCVALSAAFLVGSAPVAPVALESAAEAGAGTLANPLGTNPLKLL 61  
DB 24 RILILVGLFLALCFMSAADMALGPARYTLSEVLA-----TIADPAAVGNQLRVVI 73

QY 62 SSLGIPVNHLEGS-----IEGSKCVA-----ELGPQAVGAVKALKALGALTVF 103  
DB 74 WDIRPIALMAVTGASLSVAGAQNTILSNPLASPTFLGISAAASFGAALALVGGVAIF 133

RESULT 7  
H87275  
thio-disulfide interchange protein, probable [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 20-Apr-2001  
C:Accession: H87275  
R:Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.; B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Hatt, D.H.; Kolon, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M. Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; UID:21173698; PMID:11259647  
A:Accession: H87275  
A>Status: preliminary

A:Molecule type: DNA  
A:Residues: 1-699 <SPO>  
A:Cross-references: GB:AE005673; NID:g13421344; PIDN:AAK22204.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CC0217

Query Match 15.1%; Score 76; DB 2; Length 699;  
Best Local Similarity 30.5%; Pred. No. 21;  
Matches 32; Conservative 18; Mismatches 37; Indels 18; Gaps 5;

QY 3 LAALLGLCVALSAAFLVGSAPVAPVALESAAEAGAGTLANPLGTNPLKLL 61  
DB 545 VSMITGLAVVAGALAAASAKP---FVAAEASTSGPGLTAE---AWSPEKVAL 598

QY 62 SSLGIPVNHLEGS-----QKCVAEILGPQAVGAVKALKALL 97  
DB 599 QAEGRPV---LVDFTAAVCVTCQVNEKVALSGPKVAEAFKAQNAVL 641

RESULT 8  
T47269  
copper-transporting ATPase (EC 3.6.1.-) P-type copA [validated] - Helicobacter felis  
C:Species: Helicobacter felis  
C:Date: 20-Apr-2000 #sequence\_revision 20-Apr-2000 #text\_change 08-Sep-2000  
C:Accession: T47269  
R:Bayle, D.; Wangier, S.; Weitzneger, T.; Steinhilber, W.; Volz, J.; Przybylski, M.; J. Bacteriol. 180, 317-329, 1998  
A:Title: Properties of the P-type ATPases encoded by the copA operons of Helicobacter  
A:Reference number: 224437; UID:98101471; PMID:9440521  
A:Accession: T47269  
A>Status: translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-732 <BAY>  
A:Cross-references: EMBL:AJ001932; NID:g2660538; PIDN:CAA05104.1; PID:g2660542  
A:Experimental source: strain ATCC 49179  
C:Genetics:  
A:Gene: copA  
C:Function:  
A:Description: binds copper specifically [validated, UID:98101471]  
A>Note: involved in copper resistance  
C:Superfamily: Enterococcus copper-transporting ATPase copA; ATPase nucleotide-binding  
C:Keywords: copper binding; hydrolase  
F:8-37/Domain: heavy-metal-associated homology <HMA>  
F:532-674/Domain: ATPase nucleotide-binding domain homology <ATN>

Query Match 15.1%; Score 76; DB 2; Length 732;  
Best Local Similarity 26.3%; Pred. No. 22;  
Matches 35; Conservative 17; Mismatches 39; Indels 42; Gaps 6;

QY 6 LLGLCVALSAAFLVGSAPVAPVAAL-----ESAAEAGAG-----45  
DB 447 LLTLCASLEAQSSEHVIAGKIVAHAKGQIALQEVQAKPGFGIKGVGDQIKAGNLE 506

QY 46 --TLANPLGTNPLKLLSS-----LGIPV--NHLEGSQKCVAEILGPQAVGA-----89  
DB 507 FPNLEPNFTGLGEGVFGTGTQILGVVVLADSLKEGSKAISEL--KALGVKTTLLSGD 564

QY 90 ----VKALKALLG 98  
DB 565 NLENVRALATQLG 577

RESULT 9  
H72647  
hypothetical protein APE0614 - Aeropyrum pernix (strain KI)  
C:Species: Aeropyrum pernix  
C:Date: 20-Aug-1999 #sequence\_revision 20-Aug-1999 #text\_change 20-Aug-1999  
C:Accession: H72647  
R:Kawarayashi, Y.; Hino, Y.; Horikawa, H.; Yamazaki, S.; Haikawa, Y.; Jin-no, K.; Takawa, H.; Takamiya, M.; Masuda, S.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; DNA Res. 6, 83-101, 1999  
A:Title: Complete genome sequence of an aerobic hyper-thermophilic Crenarchaeon, Aeropyrum pernix  
A:Reference number: A72450; UID:99310339; PMID:10382966

A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-502 <STO>  
A:Cross-references: GB:AE004509; GB:AE004622; PIDN:AAG04136.1; GSPDB:GN00  
A:Experimental source: strain PA01  
C:Genetics:  
A:Gene: PA0747  
C:Superfamily: aldehyde dehydrogenase (NAD+); aldehyde dehydrogenase homology

Query Match 14.5%; Score 73; DB 2; Length 502;  
Best Local Similarity 29.1%; Pred. No. 29;  
Matches 32; Conservative 13; Mismatches 41; Indels 24; Gaps 5;

QY 4 AALGLCVALSCTSA-----AAFLVGSAX-----PVAQPVAALESA-----AEAGAGTL 47  
DB 264 ACVLGNLVGSCGAAGORCAISAAVFGAARWIPELAEKMAVLDPGHQDPDDAAYGLP 323  
QY 49 ANPLGTINPLKLLSLGIPVNHLEGSQKCVAE-----LQPGAVGAV 90  
DB 324 ISPGARQVRLIEAGKAEACILDSQ-CQVEGYPNGNLGPTLFRV 372

RESULT 12  
B87315  
gamma-glutamyltransferase [imported] - Caulobacter crescentus  
C:Species: Caulobacter crescentus  
C:Date: 20-Apr-2001 #sequence\_revision 20-Apr-2001 #text\_change 10-May-2001  
C:Accession: B87315  
B; Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.  
B; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kol  
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.  
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001  
A:Title: Complete Genome Sequence of Caulobacter crescentus.  
A:Reference number: A87249; MUID:21173698; PMID:11259647  
A:Accession: B87315  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-584 <STO>  
A:Cross-references: GB:AE005673; NID:gl3421716; PIDN:AAK22518.1; GSPDB:GN00148  
C:Genetics:  
A:Gene: CC0531  
C:Superfamily: gamma-glutamyltransferase

Query Match 14.5%; Score 73; DB 2; Length 584;  
Best Local Similarity 28.6%; Pred. No. 34;  
Matches 28; Conservative 10; Mismatches 38; Indels 22; Gaps 2;

QY 2 KLAALGLCVALSCTSAAFILVGSAPVQPV--AALESAEAGAGTLANPLGTINPLKL 59  
DB 7 RLASLLASAAQLSLAPVAALAESIPLAMPTPRPAATSTPAKGMVAANFLAVEAGLRV 66  
QY 60 LLSSLGIPVNHLEGSQKCVAEELGPQAVGAVKALKALL 97  
DB 67 LRD-----GGSAVDAVAIQAVL 84

RESULT 13  
TL3613  
hypothetical protein sp8.2 - fruit fly (Drosophila melanogaster)  
C:Species: Drosophila melanogaster  
C:Date: 13-Aug-1999 #sequence\_revision 13-Aug-1999 #text\_change 17-Nov-2000  
C:Accession: TL3613  
R; Papagiannakis, G.; Spanos, I.; Cox, S.; Siden-Kiamos, I.; Louis, C.  
submitted to the EMBL Data Library, April 1999  
A:Description: Sequencing the distal X chromosome of Drosophila melanogaster.  
A:Reference number: Z17695  
A:Accession: TL3613  
A>Status: preliminary; translated from GB/EMBL/DBJ  
A:Molecule type: DNA  
A:Residues: 1-1279 <PAP>  
A:Cross-references: EMBL:AL020218; NID:e1273253; PID:e1426350; PIDN:CAA17685.2  
C:Genetics:  
A:Cross-references: FlyBase:FBgn0024367

```
A;Introns: 65/2
A;Note: EG:8D8.2

Query Match      14.5%; Score 73; DB 2; Length 1279;
Best Local Similarity 31.6%; Pred. No. 75;
Matches 31; Conservative 12; Mismatches 29; Indels 26; Gaps 4;

QY 25 SAKPVAQPVALESA-----AAAGAGTLANPLGTLNPKLLSSLGIPVN 69
DB 213 SANPAAPSAARFSSHYSAKNAQFURKPKPSGGGSLSS---TVKPVADILESIGVSG 269
QY 70 HLJEGSQK-----CVAEIGQPQ-AVGAVKALKALIGA 99
DB 270 GKSDSAHKRYALDDYYPAESAPQSPVAVADLRGLHGA 307

RESULT 14
A56010
amastigote-specific protein A2 precursor - Leishmania donovani infantum
C;Species: Leishmania donovani infantum
C;Date: 28-Apr-1995 #sequence_revision 28-Apr-1995 #text_change 24-Nov-1999
C;Accession: A56010
R;Charest, H.; Matlashewski, G. 1994
Mol. Cell. Biol. 14, 2975-2984, 1994
A;Title: Developmental gene expression in Leishmania donovani: differential cloning and
A;Reference number: A56010; MUID:94217695; PMID:7545921
A;Accession: A56010
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-236 <CHA>
A;Cross-references: GB:S69693; NID:G546453; PID:G546454
C;Superfamily: proline-rich protein
C;Keywords: tandem repeat

Query Match      14.3%; Score 72; DB 2; Length 236;
Best Local Similarity 29.8%; Pred. No. 17;
Matches 31; Conservative 15; Mismatches 42; Indels 16; Gaps 4;

QY 1 MKLAALLGLCVALLSCSSAAAFVLSGAKP--VAQPVALESAAEAGAGTLANPLGTLNPLK 58
DB 1 MKIRSVRLVLLVCAVLAALSASAEHPKAAVDVGPL-SVGPSVGSLPSVGPQAVGPLS 59
QY 59 LLLSSLGIPVNHLEGSQKCVAEIGQPQAVGAVKALKALIGALT 102
DB 60 VGPSQSVG-FLS-----VGQPAVGPLSVGQSVGPLSV 90

RESULT 15
AE2900
succinyl-CoA synthetase beta chain [imported] - Agrobacterium tumefaciens (strain C58, D
C;Species: Agrobacterium tumefaciens
C;Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C;Accession: AE2900
R;Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I.;
Erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavina, T.; Levy, R.; Li, M.; McClellan;
Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A;Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, M.; Perry, M.; Gordon-Kamm,
ster, B.W.
A;Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A;Reference number: AB2577; MUID:21608550; PMID:11743193
A;Accession: AE2900
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <KUR>
A;Cross-references: GB:AE008688; PIN:AA43619.1; PID:g17741140; GSPDB:GN00186
A;Experimental source: strain C58 (Dupont)
C;Genetics:

A;Gene: succ
A;Map position: circular chromosome
C;Superfamily: succinate-CoA ligase (ADP-forming) beta chain

Query Match      14.3%; Score 72; DB 2; Length 397;

Best Local Similarity 36.2%; Pred. No. 28;
Matches 29; Conservative 8; Mismatches 31; Indels 12; Gaps 4;

QY 18 AAFLVGSAGKPVQVAALAE-SAAEAGAGTLANPLGTLNPKLLSSLGIPVNHLEGSQ 76
DB 8 AKALLKGYGAPVAEGVAILKVEEAFAAAKQLPGPLYV---VKSQIHAGG-----RKKG 57
QY 77 KCVAEIGQPQAVGAVKALKAL 96
DB 58 K-FKELGPDPAKGGVRLAKSI 76

RESULT 16
F97675
succinyl-CoA synthetase beta chain (AF326913) [imported] - Agrobacterium tumefaciens (
C;Species: Agrobacterium tumefaciens
C;Date: 30-Sep-2001 #sequence_revision 30-Sep-2001 #text_change 18-Nov-2002
C;Accession: F97675
R;Goodner, B.; Hinkle, G.; Gattung, S.; Miller, N.; Blanchard, M.; Qurollo, B.; Goldma
A.; Liu, F.; Wollam, C.; Allinger, M.; Doughty, D.; Scott, C.; Lappas, C.; Markelz, B
Science 294, 2323-2328, 2001
A;Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium t
A;Reference number: A97359; MUID:21608551; PMID:11743194
A;Accession: F97675
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-397 <KUR>
A;Cross-references: GB:AE007869; PID:AAK88359.1; PID:g15157842; GSPDB:GN00169
A;Genetics:
A;Gene: AGR_C_4780
A;Map position: circular chromosome
C;Superfamily: succinate-CoA ligase (ADP-forming) beta chain

Query Match      14.3%; Score 72; DB 2; Length 397;
Best Local Similarity 36.2%; Pred. No. 28;
Matches 29; Conservative 8; Mismatches 31; Indels 12; Gaps 4;

QY 18 AAFLVGSAGKPVQVAALAE-SAAEAGAGTLANPLGTLNPKLLSSLGIPVNHLEGSQ 76
DB 8 AKALLKGYGAPVAEGVAILKVEEAFAAAKQLPGPLYV---VKSQIHAGG-----RKKG 57
QY 77 KCVAEIGQPQAVGAVKALKAL 96
DB 58 K-FKELGPDPAKGGVRLAKSI 76

RESULT 17
D70968
hypothetical protein RV2672 - Mycobacterium tuberculosis (strain H37RV)
C;Species: Mycobacterium tuberculosis
C;Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C;Accession: D70968
R;Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon,
; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd,
Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A;Authors: Sgares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A;Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genom
A;Reference number: A70500; MUID:98295987; PMID:9634230
A;Accession: D70968
A;Status: preliminary; nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-528 <COL>
A;Cross-references: GB:Z80225; GB:AL123456; NID:g3242265; PID:CAE02326.1; PID:e266414
A;Experimental source: strain H37RV
C;Genetics:
A;Gene: RV2672

Query Match      14.3%; Score 72; DB 2; Length 528;
Best Local Similarity 28.4%; Pred. No. 38;
Matches 29; Conservative 15; Mismatches 34; Indels 24; Gaps 4;

QY 3 LAALLGLCVALLSCSSAAAFVLSGAKPVQVALESAAEAGAG-----TLANPLGTLN 55
```

```
Db 300 LDFAAACVAVNCA-----LGSHPKGA--VSALLSAARSGDGPGGASVAAVANAVAT-- 349
QY 56 PLKLLSSLGIPVNHLEGSQKCVAEELGPOAVGAVKALKALL 97
Db 350 -----ALGFPDSGRVDSITTKLADALAAARSGDMNLSALI 384

RESULT 18
B87634
L-serine dehydratase [imported] - Caulobacter crescentus
C:Species: Caulobacter crescentus
C>Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 10-May-2001
C:Accession: B87634
R:Bernier, W.C.; Felldbylum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.
B.; Laub, M.T.; DeBoy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
A:Title: Complete Genome Sequence of Caulobacter crescentus.
A:Reference number: A87249; MUID:21173699; PMID:11259647
A:Accession: B87634
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-462 <STO>
A:Cross-references: GB:AE005673; NID:G13424766; PIDN:AAK25070.1; GSPDB:GN00148
C:Genetics:
A:Gene: CC3108
C:Superfamily: microbial L-serine dehydratase

Query Match 14.2%; Score 71.5; DB 2; Length 462;
Best Local Similarity 31.2%; Pred. No. 37;
Matches 30; Conservative 12; Mismatches 21; Indels 33; Gaps 6;
QY 11 VALSCSAAFLVGSAPVAPVAALESAAEAG-----AGTLNPLGTLPNPLKLLSSSLGI 66
Db 347 VGVACSWAAA---GLAALGGTNAQIENAAEIGWENLGLTCDPIGGL-----VOI 394
QY 67 PVNHLEGSQKCVAEELGPOAVGAVKALK-----ALLG 98
Db 395 P-----CIER---NANGAIKADAARLALLG 417

RESULT 19
AC3070
ATP-dependent Clp proteinase, ATP-binding subunit clpB [imported] - Agrobacterium tumefa
C:Species: Agrobacterium tumefaciens
C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
C:Accession: AC3070
R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, I
erage, G.; Gillet, W.; Grant, C.; Guenther, D.; Kutyavin, T.; Levy, R.; Li, M.; McClell
; Karp, P.; Romero, P.; Zhang, S.
Science 294, 2317-2323, 2001
A:Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krespan, W.; Perry, M.; Gordon-Kamm,
ster, E.W.
A:Reference number: AB2577; MUID:21608550; PMID:11743193
A:Accession: AC3070
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-874 <KUR>
A:Cross-references: GB:AE008689; PIDN:AAL44977.1; PID:G17742634; GSPDB:GN00187
A:Experimental source: strain C58 (Dupont)
C:Genetics:
A:Gene: clpB
A:Map position: linear chromosome
C:Superfamily: endopeptidase Clp ATP-binding chain

Query Match 14.2%; Score 71.5; DB 2; Length 874;
Best Local Similarity 26.1%; Pred. No. 70;
Matches 23; Conservative 23; Mismatches 37; Indels 5; Gaps 2;
QY 18 AAFLVGSAPVAPVAALESAAEAGAGTLPNPLKLLSS-LGIPVNHLEGSQ 76

RESULT 20
F98216
endopeptidase clp ATP-binding chain B [imported] - Agrobacterium tumefaciens (strain C5
C:Species: Agrobacterium tumefaciens
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 18-Nov-2002
C:Accession: F98216
R:Goodner, B.; Hinkle, G.; Gattung, S.; Maller, N.; Blanchard, M.; Qurollo, B.; Goldman
A.; Liu, F.; Wollan, C.; Allinger, M.; Dougherty, D.; Scott, C.; Lappas, C.; Markelz, B.
Science 294, 2323-2328, 2001
A:Title: Genome Sequence of the Plant Pathogen and Biotechnology Agent Agrobacterium tu
A:Reference number: A97359; MUID:21608551; PMID:11743194
A:Accession: F98216
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-887 <KUR>
A:Cross-references: GB:AE007870; PIDN:AAK99256.1; PID:G15159084; GSPDB:GN00170
C:Genetics:
A:Gene: AGR_L1346
A:Map position: linear chromosome
C:Superfamily: endopeptidase Clp ATP-binding chain

Query Match 14.2%; Score 71.5; DB 2; Length 887;
Best Local Similarity 26.1%; Pred. No. 71;
Matches 23; Conservative 23; Mismatches 37; Indels 5; Gaps 2;
QY 18 AAFLVGSAPVAPVAALESAAEAGAGTLPNPLKLLSS-LGIPVNHLEGSQ 76
Db 512 AGELTYGIIPGLEKELAAAEARDSSGAGSMVQEVVTPDNIAHVSVRWGTGIPVDKLEQGR 571
QY 77 KCVA-----ELGPOAVGAVKALKALL 100
Db 572 EKLLRMEDELAKEVWGQGEAVQAVSKAV 599

RESULT 21
C83368
probable MFS transporter PA2214 [imported] - Pseudomonas aeruginosa (strain PAO1)
C:Species: Pseudomonas aeruginosa
C>Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C83368
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrenner, P.; Hickey, M.J.; B
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim
; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic path
A:Reference number: A82950; MUID:20437337; PMID:10984043
A:Accession: C83368
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-440 <STO>
A:Cross-references: GB:AE004648; GB:AE004091; NID:G9948237; PIDN:AAG05602.1; GSPDB:GN00
C:Genetics:
A:Gene: PA2214

Query Match 14.1%; Score 71; DB 2; Length 440;
Best Local Similarity 32.7%; Pred. No. 39;
Matches 36; Conservative 7; Mismatches 45; Indels 22; Gaps 5;
QY 3 LAALLGLCVALSASSAAFLVGSAPV--AQPVALESAAEAGAGTLPNPLGTIN----- 55
Db 333 LAGNLGIAVIAFCFAASGVF--SVQPLFTLTPTGYLSGAAASGIALINSLGNLGGFVAP 390
QY 56 PLKLLSSLGIPVNHLEGSQKCVAEELGPOAVGAVKALK-LIGALTVPFG 104
Db 391 NLKTIME-----SQFADPRAGMFAAAGVLLGACLLARLKTSG 428
```

## RESULT 22

G85160  
heat shock protein like [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 17-May-2002  
C:Accession: G85160  
R:anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring  
Nature 402, 769-777, 1999  
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.  
A:Reference number: A85001; MUID:20083488; PMID:10617198  
A:Accession: G85160  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-668 <STO>  
A:Cross-references: GB:NC\_001268; NID:g5302773; PIDN:CAB46061.1; GSPDB:GN00140  
C:Genetics:  
A:Gene: dl3375w  
A:Map position: 4  
C:Superfamily: endopeptidase Clp ATP-binding chain

Query Match 14.0%; Score 70.5; DB 2; Length 668;  
Best Local Similarity 27.6%; Pred. No. 66;  
Matches 24; Conservative 17; Mismatches 41; Indels 5; Gaps 2;

QY 18 AAFLVGSAPVQAQVVALESAAEAGAGTLANPLGTLNPLKLLSSLGIPVNHLEGSQK 77  
DB 465 AAVLKYGAIQVESIAKLESAKDNV-MLTETVGPENIAEVSVSWTGPVTRLDQNEKK 523

QY 78 CVAELG----PQAVGAVKALKALLGAL 100

DB 524 RLISLADKLHERVVGQDEAVKAAVAAI 550

## RESULT 23

D71409  
Probable endopeptidase Clp ATP-binding chain - Arabidopsis thaliana  
N:Alternate names: ATP-dependent Clp proteinase regulatory chain  
N:Contains: adenosinetriphosphatase (EC 3.6.1.3)  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
A:Variety: Columbia  
C:Date: 03-Aug-1998 #sequence\_revision 03-Aug-1998 #text\_change 19-Jan-2001  
R:Bevan, M.; Bancroft, I.; Bent, E.; Love, K.; Goodman, H.; Dean, C.; Bergkamp, R.; Dirk  
P.; Wedler, H.; Wedler, E.; Wambutt, R.; Weitzenegger, T.; Pohl, T.M.; Teryn, N.; Giel  
avanagh, T.; Hempel, S.; Kotter, P.; Entian, K.D.; Rieger, M.; Schaeffer, M.; Funk, B.  
Nature 391, 485-488, 1998  
A:Authors: Mueller-Auer, S.; Silvey, M.; James, R.; Montfort, A.; Pons, A.; Puigdomenech  
erhoft, A.; Moores, T.; Jones, J.D.G.; Eneva, T.; Palme, K.; Benes, V.; Rechman, S.; Ans  
C.; Chalwatzis, N.  
A:Title: Analysis of 1.9 Mb of contiguous sequence from chromosome 4 of Arabidopsis thal  
A:Reference number: A71400; MUID:98121113; PMID:9461215  
A:Accession: D71409  
A:Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-831 <BEV>  
A:Cross-references: GB:D97336; NID:g2244788; PIDN:CAB10246.1; PID:g2244823  
C:Genetics:  
A:Map position: 4COP9-4Q3845  
C:Function:

A:Description: allows clipp to hydrolyze polypeptides and proteins, probably by a chaperon  
e activity; ATP hydrolysis is required for Clp hydrolysis of proteins but not of smaller  
C:Superfamily: endopeptidase Clp ATP-binding chain  
C:Keywords: ATP; hydrolase; molecular chaperone; nucleotide binding; P-loop  
F:172-179/Region: nucleotide-binding motif A (P-loop)  
F:240-245/Region: nucleotide-binding motif B  
F:571-578/Region: nucleotide-binding motif A (P-loop)  
F:640-645/Region: nucleotide-binding motif B  
F:178/Binding site: ATP (Lys) #status predicted  
F:577/Binding site: ATP (Lys) #status predicted

Query Match 14.0%; Score 70.5; DB 2; Length 831;

Best Local Similarity 27.6%; Pred. No. 83;  
Matches 24; Conservative 17; Mismatches 41; Indels 5; Gaps 2;

QY 18 AAFLVGSAPVQAQVVALESAAEAGAGTLANPLGTLNPLKLLSSLGIPVNHLEGSQK 77  
DB 465 AAVLKYGAIQVESIAKLESAKDNV-MLTETVGPENIAEVSVSWTGPVTRLDQNEKK 523  
QY 78 CVAELG----PQAVGAVKALKALLGAL 100  
DB 524 RLISLADKLHERVVGQDEAVKAAVAAI 550

## RESULT 24

C86178  
hypothetical protein [imported] - Arabidopsis thaliana  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 02-Mar-2001 #sequence\_revision 02-Mar-2001 #text\_change 31-Mar-2001  
C:Accession: C86178  
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alons  
ansen, N.F.; Hughes, B.; Huizar, L.  
Nature 408, 816-820, 2000  
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim,  
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzial  
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.  
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallon  
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.  
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.  
A:Reference number: A86141; MUID:21016719; PMID:11130712  
A:Accession: C86178  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-431 <STO>  
A:Cross-references: GB:AE005172; NID:g2494120; PIDN:AA80629.1; GSPDB:GN00141  
C:Genetics:  
A:Map position: 1

Query Match 13.9%; Score 70; DB 2; Length 431;  
Best Local Similarity 28.2%; Pred. No. 47;  
Matches 35; Conservative 15; Mismatches 50; Indels 24; Gaps 4;

QY 3 LAALLGCLVALSCSAAAFVLSAKPVAQVVALESAAEA-GAGTLANPLGTLNPLKLL 61  
DB 122 LGNLLGGLLTATPPKISFLVPSALLSLQLVSLSSKEESFGLPRIAETSSVLSVKKQI 181  
QY 62 SSF-----GIPVNHLEGSQK-----VAELGPAQVGAVKAL-KALLG 98  
DB 182 SNLKEAIQADEISQPLINAVVSIAMVPLLSGVFCYQTVLNLDPSVIGMSKVIGQLMLL 241  
QY 99 ALTIV 102  
DB 242 CLTV 245

## RESULT 25

T46147  
zinc finger protein - Arabidopsis thaliana  
N:Alternate names: protein T3A5.80  
C:Species: Arabidopsis thaliana (mouse-ear cross)  
C:Date: 04-Feb-2000 #sequence\_revision 04-Feb-2000 #text\_change 04-Feb-2000  
C:Accession: T46147  
R:Blöcker, H.; Mewes, H.W.; Mayer, K.F.X.; Lemcke, K.; Schueller, C.; Quetier, F.; Sa  
submitted to the Protein Sequence Database, December 1999  
A:Reference number: Z23024  
A:Accession: T46147  
A:Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-452 <ELO>  
A:Cross-references: EMBL:AL132999  
A:Experimental source: cultivar Columbia; BAC clone T3A5  
C:Genetics:  
A:Map position: 3  
A:Introns: 44/1; 176/2; 243/1

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Superfamily: Synchocystis hypothetical protein slr1977

Query Match 13.8%; Score 69.5; DB 2; Length 452;  
Best Local Similarity 26.9%; Pred. No. 50;  
Matches 28; Conservative 21; Mismatches 37; Indels 18; Gaps 5;

QY 9 LCVALSCTAAFLVGS-----AKPVAQPVAALESAAEAGA-----GTLNPLGLTLPKLL 60  
DB 303 ISLSTSHGSEFL-GSNRFHAFAMATALLQAAQMGAAAGGSLHGLG-----I 354  
QY 61 LSSLGIPVNHLEIGSKVCAELGPQAVGAVKALKALLGALTTFG 104  
DB 355 VSSSTSTSDAIVPHGLGLGFLPCGSESSGLKEL--MWGNSSVFG 396

RESULT 26  
D82179  
probable multidrug transporter VC1597 [imported] - Vibrio cholerae (strain N16961 serogroup O1)  
C:Species: Vibrio cholerae  
C:Date: 18-Aug-2000 #sequence\_revision 20-Aug-2000 #text\_change 06-Jan-2003  
C:Accession: D82179  
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Winn, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Baas, S.; Qin, H.; Dragoi, I.; Sellers, P. L. R.; Mekalanos, J.J.; Venter, J.C.; Fraser, C.M.  
Nature 406, 477-483, 2000  
A:Title: DNA sequence of both chromosomes of the cholera pathogen Vibrio cholerae.  
A:Reference number: A82035; MUID:20406833; PMID:10952301  
A:Accession: D82179  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-477 <HEI>  
A:Cross-references: GB:AB004237; GB:AB003852; NID:G9656107; PIDN:AAF94751.1; GSPDB:GN001  
A:Experimental source: serogroup O1; strain N16961; biotype El Tor  
C:Genetics:  
A:Gene: VC1597  
A:Map position: 1  
C:Superfamily: multidrug-efflux transporter

Query Match 13.9%; Score 70; DB 2; Length 477;  
Best Local Similarity 28.1%; Pred. No. 53;  
Matches 38; Conservative 16; Mismatches 39; Indels 42; Gaps 8;

QY 2 KLALLGLCVALSCTAAFLVGSAAKPVAALESAAEAGAAGTL----- 47  
DB 332 KFLPVFGMSLS-SCAFVLAFLSAPVVSAAIAL--CGLGSTVWFSTQVLVQTLAGK 387  
QY 48 ANPLGLTLPKLLLSLLGIPVNHLEIGS-----OKCVAELGPQA----- 86  
DB 388 AN-LGRITAMASLSLSGASVTGTAFFGTLIYSLPLGLSPNSGLQATAAL-PQSEILHAFQ 445

QY 87 VG-AVKALKALLGAL 100  
DB 446 IGFAVALLALLGAL 460

RESULT 27  
S75653  
hypothetical protein slr1977 - Synchocystis sp. (strain PCC 6803)  
C:Species: Synchocystis sp.  
A:Variety: PCC 6803  
C:Date: 25-Apr-1997 #sequence\_revision 25-Apr-1997 #text\_change 20-Jun-2000  
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda  
DNA Res. 3, 109-136, 1996  
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synchocystis sp.  
A:Reference number: S74322; MUID:97061201; PMID:8905231  
A:Accession: S75653  
A>Status: nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-244 <KAN>  
A:Cross-references: EMBL:D90912; GB:AB001339; NID:G1653228; PIDN:BA18214.1; PID:G1653228

A>Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996  
C:Superfamily: Synchocystis hypothetical protein slr1977

Query Match 13.8%; Score 69.5; DB 2; Length 244;  
Best Local Similarity 31.2%; Pred. No. 30;  
Matches 30; Conservative 11; Mismatches 30; Indels 25; Gaps 5;

QY 17 SAAFLVGSAAKPVAALESAAEAGAAGTLANPL-----GTLNPLKLLSSLGI 66  
DB 160 NTAFLAFGAQKI--DVALLRVSD-----TWTQDLPDLNGVFTGQALQPLPLAKALLR 213  
QY 67 PV--NHLIEGSKVCAELGPQAVGAVKALKALLGAL 100  
DB 214 PLAAGHLIOGSLKACQALTAIA-----QSLSGAL 242

RESULT 28  
G75454  
hypothetical protein - Deinococcus radiodurans (strain R1)  
C:Species: Deinococcus radiodurans  
C:Date: 03-Dec-1999 #sequence\_revision 03-Dec-1999 #text\_change 31-Mar-2000  
C:Accession: G75454  
R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.; M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Usterback, T.; Zalewski, C.; M. S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.  
Science 286, 1571-1577, 1999  
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.  
A:Reference number: A75250; MUID:20036896; PMID:10567266  
A:Accession: G75454  
A>Status: preliminary  
A:Molecule type: DNA  
A:Residues: 1-396 <WHI>  
A:Cross-references: GB:AE001948; GB:AE00513; NID:G6458680; PIDN:AAF10540.1; PID:G64586  
A:Experimental source: strain R1  
C:Genetics:  
A:Gene: DR0960  
A:Map position: 1

Query Match 13.8%; Score 69.5; DB 2; Length 396;  
Best Local Similarity 32.1%; Pred. No. 48;  
Matches 34; Conservative 18; Mismatches 33; Indels 21; Gaps 5;

QY 3 LAALLGLCVALSCTAAFLVGSAAKPV-AQPVALESAAEAGAAGTLANPLGLTLPKLL 61  
DB 38 LAGSAGWPAGAAQSAFAVRLPSARVPAALPVNAPAAAPSGLPASLLSSLSLNL-- 95  
QY 62 SSLGIPVNHLEIGSKC-VAELGPQAV-----GAVKALKALLG 98  
DB 96 ----IPI-----GSERLVILGVAPDALAGTPGNPGQALLAVRGVGG 132

RESULT 29  
C70582  
probable PPE protein - Mycobacterium tuberculosis (strain H37RV)  
C:Species: Mycobacterium tuberculosis  
C:Date: 17-Jul-1998 #sequence\_revision 17-Jul-1998 #text\_change 22-Oct-1999  
C:Accession: C70582  
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, J.; Connor, R.; Davies, R.; Devlin, K.; Feltwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.  
Nature 393, 537-544, 1998  
A:Authors: Squares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrrell, B.G.  
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome  
A:Reference number: A70500; MUID:98295987; PMID:9634230  
A:Accession: C70582  
A>Status: preliminary; nucleic acid sequence not shown; translation not shown  
A:Molecule type: DNA  
A:Residues: 1-423 <COL>  
A:Cross-references: GB:Z95210; GB:AL123456; NID:G3261757; PIDN:CAB08513.1; PID:E315217,  
A:Experimental source: strain H37RV  
C:Genetics:  
A:Gene: PPE

```
Query Match      13.8%; Score 69.5; DB 2; Length 423;
Best Local Similarity 31.8%; Pred. No. 52;
Matches 28; Conservative 12; Mismatches 37; Indels 11; Gaps 3;

QY 16 SGAALFLVGSAPV-----AQPVALESAAEAGAGTLANPLGTL-----NPLKLLSSLG 65
DB 158 SAASALPFTFPVQGTGPGAPAAATAAQAGAGAVADAQATLAQLPPGILSDILSALA 217
QY 66 IPVNHIEGSKQVLAELGPQAVGAVKAL 93
DB 218 ANADPLTSLGLGIATLNPQ-VGSAQPI 244

RESULT 30
AD0782
C:Species: Salmonella enterica subsp. enterica serovar Typhi
A:Note: this species has also been called Salmonella typhi
C:Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 18-Nov-2002
A:Accession: AD0782
R:Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher,
  Th, T.; Connor, F.; Cronin, A.; Davies, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar,
  S.; Moule, S.; O'Garra, P.
Nature 413, 848-852, 2001
A:Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
  A:Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
  A:Reference number: AB0502; UID:21534947; PMID:11677608
A:Accession: AD0782
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-455 <PAR>
A:Cross-references: GB:AL513382; PIDN:CAD02578.1; PID:g16503436; GSPDB:GN00176
C:Genetics:
A:Gene: STV2430
C:Superfamily: microbial L-serine dehydratase
C:Keywords: ammonia-lyase; carbon-nitrogen lyase; carbon-oxygen lyase; hydro-lyase

Query Match      13.8%; Score 69.5; DB 2; Length 455;
Best Local Similarity 29.0%; Pred. No. 56;
Matches 31; Conservative 17; Mismatches 26; Indels 33; Gaps 7;

QY 4 AALLGL--C---VALSCSAA---AFLVGSAPVQAPVALESAAEAGAGTLANPLGTL 54
DB 329 ASILGSEVGCGSIGVACNSAAGLAELMGAS--VEQTLSAEIAMEHHLGTCPLG-- 384
QY 55 NPLKLLSSIGIPVNHIEGSKQVLAELGPQAVGAVKALKALGALT 101
DB 385 -----GQVQIP-----CIER---NAISAVKAINAATMAMS 411

RESULT 31
AF3312
hypothetical protein BMEI0484 [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002
A:Accession: AF3312
R:DelVecchio, V.G.; Kapral, V.; Redkar, R.J.; Patra, G.; Muter, C.; Los, T.; Ivanova,
  Mazur, M.; Gotsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
  Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitens
  A:Reference number: AD3252; PMID:11756688
A:Accession: AF3312
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-170 <KUR>
A:Cross-references: GB:AE008917; PIDN:AAL51665.1; PID:g17982396; GSPDB:GN00190
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0484
A:Map position: 1

Query Match      13.7%; Score 69; DB 2; Length 170;
Best Local Similarity 29.8%; Pred. No. 23;

Matches 31; Conservative 14; Mismatches 45; Indels 14; Gaps 5;

QY 6 LLGLCVALSAAFLVGSAPVQAPVALESAAEAGAGTLANPLGTLNPLKLLSSL- 64
DB 2 LAGLAAACNSTESALDIQGSNKDTGQ--AATTAPSNAPVATPPAPQRAILKPKGLHIPIV 59
QY 65 GIPVN-----HLIEGSKQVLA-ELG-----PQAVGAVKALKAL 97
DB 60 GAPVNVVTPLTTHRMNDKAMGIELAGNNDPSAAAYVIKGYFSVL 103

RESULT 32
D75393
serine proteinase, subtilase family - Deinococcus radiodurans (strain R1)
C:Species: Deinococcus radiodurans
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
A:Accession: D75393
R:White, C.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
  M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.;
  S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
  A:Reference number: A75250; UID:20036896; PMID:10567266
A:Accession: D75393
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-627 <WHI>
A:Cross-references: GB:AE001990; GB:AE000513; NID:G6459214; PIDN:AAF11026.1; PID:G6459
A:Experimental source: strain R1
C:Genetics:
A:Gene: DR1459
A:Map position: 1

Query Match      13.7%; Score 69; DB 2; Length 627;
Best Local Similarity 31.1%; Pred. No. 86;
Matches 32; Conservative 14; Mismatches 39; Indels 18; Gaps 5;

QY 2 KLAALIGLCVALSCSAAFLVGSAPVQAPVALESAAEAGAGTLANPLGTLNPLKLL 61
DB 6 KLTLTLLGALALUSQASQAS--AGSLSP-----TLQKARAGDQT---PIGVIVRFNVAN 54
QY 62 SSLIGIPVNHIEGSKQVLAELGP-----QAVGAVKALKAL 97
DB 55 TAQGRALFKNLRGQLNSQIAKLGPSAGFLKQAVNSQKATQLWL 97

RESULT 33
T36551
probable ATP-dependent proteinase ATP-binding chain - Streptomyces coelicolor (fragmen
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Feb-2001
A:Accession: T36551
R:Murphy, L.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
  submitted to the EMBL Data Library, May 1999
A:Reference number: Z21609
A:Accession: T36551
A>Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: DNA
A:Residues: 1-853 <YUR>
A:Cross-references: EMBL:AL049754; PIDN:CAB42048.1; GSPDB:GN00070; SCOEDB:SCH10.39C
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: clpB; SCOEDB:SCH10.39C
C:Superfamily: endopeptidase Clp ATP-binding chain
C:Keywords: ATP; molecular chaperone; nucleotide binding; P-loop
F:195-202/Region: nucleotide-binding motif A (P-loop)
F:276-281/Region: nucleotide-binding motif B
F:597-604/Region: nucleotide-binding motif A (P-loop)
F:665-670/Region: nucleotide-binding motif B
F:201/Binding site: ATP (Lys) #status predicted
F:603/Binding site: ATP (Lys) #status predicted

Query Match      13.7%; Score 69; DB 2; Length 853;
```



Db 782 RVPR-----GRLTVVLGPTGSGKSTLLDALICAV 812

## RESULT 38

Sl6296  
ferric enterobactin transport protein fepD - Escherichia coli (strain K-12)  
N;Alternate names: ferricenterobactin permease fepD  
C;Species: Escherichia coli  
C;Date: 04-Dec-1992 #sequence\_revision 04-Dec-1992 #text\_change 01-Mar-2002  
C;Accession: Sl6296; Sl6305; D64792; Sl4841  
R;Shea, C.M.; McIntosh, M.A.  
Mol. Microbiol. 5, 1415-1428, 1991  
A;Title: Nucleotide sequence and genetic organization of the ferric enterobactin transp  
A;Reference number: Sl6295; MUID:92157868; PMID:1838574  
A;Accession: Sl6296  
A;Molecule type: DNA  
A;Residues: 1-334 <SHE>  
A;Cross-references: EMBL:X57471; NID:G41429; PIDN:CRAA0707.1; PID:G41430  
R;Chenault, S.S.; Earhart, C.F.  
Mol. Microbiol. 5, 1405-1413, 1991  
A;Title: Organization of genes encoding membrane proteins of the Escherichia coli ferric  
A;Reference number: Sl6305; MUID:92157867; PMID:1787794  
A;Accession: Sl6305  
A;Molecule type: DNA  
A;Residues: 1-232, 'AL', 235-334 <CHE>  
A;Cross-references: EMBL:X59402; NID:G41433; PIDN:CRAA2043.1; PID:G41434  
R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co  
A.; Rose, D.J.; Mau, B.; Shao, Y.  
Science 277, 1453-1462, 1997  
A;Title: The complete genome sequence of Escherichia coli K-12.  
A;Reference number: A64720; MUID:97426617; PMID:9278503  
A;Accession: D64792  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-334 <BLAT>  
A;Cross-references: GB:AE000164; GB:U00096; NID:G1786800; PIDN:AAC73691.1; PID:G1786805;  
A;Experimental source: strain K-12, substrain MG1655  
C;Genetics:  
A;Gene: fepD  
A;Map position: 14 min  
A;Superfamily: vitamin B12 transport protein btuC  
C;Keywords: transmembrane protein  
F;16-32/Domain: transmembrane #status predicted <TM1>  
F;65-81/Domain: transmembrane #status predicted <TM2>  
F;94-110/Domain: transmembrane #status predicted <TM3>  
F;121-137/Domain: transmembrane #status predicted <TM4>  
F;156-172/Domain: transmembrane #status predicted <TM5>  
F;198-214/Domain: transmembrane #status predicted <TM6>  
F;240-256/Domain: transmembrane #status predicted <TM7>  
F;284-300/Domain: transmembrane #status predicted <TM8>  
F;310-326/Domain: transmembrane #status predicted <TM9>

Query Match 13.5%; Score 68; DB 2; Length 334;  
Best Local Similarity 22.1%; Pred. No. 56;  
Matches 34; Conservative 19; Mismatches 43; Indels 59; Gaps 6;  
Qy 3 LAALLGLCVALS-----SAAFLVGS-----KPAQP----- 32  
Db 41 LEAFSGTCQADCTIVLDARLPRTLGLAGGALGALMOTLRNPLADPGLLVNAG 100  
Qy 33 -----VAALSAEAGAGTIANPL-----GTLNPKLLLSLGIPIV 68  
Db 101 ASFAIVLGAALFGYSSAQEQQLAMAFAGALVASLIVAFSGGGQLSPVRLTLA--GVAL 158

Qy 69 NHLIEGSKVAGLGPQAVGAVKALLGALTIV 102  
Db 159 AAVLEGLTSGIALLNPVDVYDQLRFWQA--GSLDI 190

## RESULT 39

A8558  
ferric enterobactin (enterochelin) transport [imported] - Escherichia coli (strain O157:  
C;Species: Escherichia coli

C;Date: 16-Feb-2001 #sequence\_revision 16-Feb-2001 #text\_change 17-May-2002  
C;Accession: A8558  
R;Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glasner, J.D.; Rose, D.J.; Mayt  
iller, L.; Grotbeck, E.J.; Davis, N.W.; Lim, A.; Dimalanta, E.; Potamousis, K.; Apodac  
Nature 409, 529-533, 2001  
A;Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.  
A;Reference number: A85480; MUID:21074935; PMID:11206551  
A;Accession: A8558  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-334 <STO>  
A;Cross-references: GB:AE005174; NID:G12513480; PIDN:AAG54925.1; GSPDB:GN00145; UWGP:Z  
A;Experimental source: strain O157:H7, substrain EDL933  
C;Genetics:  
A;Gene: fepD  
C;Superfamily: vitamin B12 transport protein btuC

Query Match 13.5%; Score 68; DB 2; Length 334;  
Best Local Similarity 22.1%; Pred. No. 56;  
Matches 34; Conservative 19; Mismatches 43; Indels 58; Gaps 6;  
Qy 3 LAALLGLCVALS-----SAAFLVGS-----KPAQP----- 32  
Db 41 LEAFSGTCQADCTIVLDARLPRTLGLAGGALGALMOTLRNPLADPGLLVNAG 100  
Qy 33 -----VAALSAEAGAGTIANPL-----GTLNPKLLLSLGIPIV 68  
Db 101 ASFAIVLGAALFGYSSAQEQQLAMAFAGALVASLIVAFSGGGQLSPVRLTLA--GVAL 158  
Qy 69 NHLIEGSKVAGLGPQAVGAVKALLGALTIV 102  
Db 159 AAVLEGLTSGIALLNPVDVYDQLRFWQA--GSLDI 190

## RESULT 40

E90707  
ferric enterobactin (enterochelin) transport ECS0629 [imported] - Escherichia coli (st  
C;Species: Escherichia coli  
C;Date: 18-Jul-2001 #sequence\_revision 18-Jul-2001 #text\_change 17-May-2002  
C;Accession: E90707  
R;Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C  
gaekawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.  
DNA Res. 8, 11-22, 2001  
A;Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and ge  
A;Reference number: A99629; MUID:21156231; PMID:11258796  
A;Accession: E90707  
A;Status: preliminary  
A;Molecule type: DNA  
A;Residues: 1-334 <HAY>  
A;Cross-references: GB:BA000007; PIDN:BA834052.1; PID:G13360087; GSPDB:GN00154  
A;Experimental source: strain O157:H7, substrain RIMD 0509952  
C;Genetics:  
A;Gene: ECS0629  
C;Superfamily: vitamin B12 transport protein btuC

Query Match 13.5%; Score 68; DB 2; Length 334;  
Best Local Similarity 22.1%; Pred. No. 56;  
Matches 34; Conservative 19; Mismatches 43; Indels 58; Gaps 6;  
Qy 3 LAALLGLCVALS-----SAAFLVGS-----KPAQP----- 32  
Db 41 LEAFSGTCQADCTIVLDARLPRTLGLAGGALGALMOTLRNPLADPGLLVNAG 100  
Qy 33 -----VAALSAEAGAGTIANPL-----GTLNPKLLLSLGIPIV 68  
Db 101 ASFAIVLGAALFGYSSAQEQQLAMAFAGALVASLIVAFSGGGQLSPVRLTLA--GVAL 158  
Qy 69 NHLIEGSKVAGLGPQAVGAVKALLGALTIV 102  
Db 159 AAVLEGLTSGIALLNPVDVYDQLRFWQA--GSLDI 190

Search completed: April 5, 2004, 14:36:01



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OM protein - protein search, using sw model

Run on: April 5, 2004, 14:11:13 ; Search time 17 Seconds  
(without alignments)  
318,547 Million cell updates/sec

Title: US-09-997-428-408

Perfect score: 502

Sequence: 1 MKLAALLGLCVLSCSSAAA.....QAVGAVKALKALIGALTVEG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters: 141681

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : SwissProt\_42.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence Comparison  
ID

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	497	99.0	104	1	UGR2_HUMAN
2	250	49.8	104	1	UGR2_MOUSE
3	160	31.9	93	1	UGR1_HUMAN
4	135	26.9	139	1	UGR1_MOUSE
5	83	16.5	127	1	TKN1_HUMAN
6	77	15.3	335	1	TRD2_STRCO
7	76	15.1	732	1	COPA_HELFE
8	75	14.9	362	1	MDC1_HUMAN
9	75	14.7	779	1	SNL1_MOUSE
10	74	14.7	779	1	SNL1_MOUSE
11	73.5	14.6	626	1	DXS_WIGBR
12	73.5	14.6	776	1	SNL1_RAT
13	73.5	14.6	882	1	SYN1_THETH
14	72	14.3	397	1	SUCC_AGR5
15	71	14.1	428	1	FXE2_MOUSE
16	71	14.1	480	1	DNAH_RHIME
17	69	13.7	124	1	RL7_RALSO
18	68.5	13.6	377	1	PROB_BIFLO
19	68	13.5	324	1	PEPD_ECOLI
20	68	13.5	589	1	SILF_MOUSE
21	67.5	13.4	2035	1	GCP_MYCLE
22	67	13.3	351	1	FUMC_PESM
23	67	13.3	464	1	TAZR_RAT
24	66.5	13.2	341	1	FXD1_HUMAN
25	66.5	13.2	465	1	NLTD_BRAOL
26	66	13.1	118	1	NP70_WYCKA
27	66	13.1	121	1	CLRC_IDEDE
28	66	13.1	239	1	PTB_MOUSE
29	66	13.1	527	1	LEU1_PROMM
30	66	13.1	540	1	LEU1_PROMM
31	66	13.1	585	1	NUPI_RAT
32	65.5	13.0	257	1	BUTC_RHOER
33	65.5	13.0	336	1	COBT_RHLO

RESULT 1

See over

34	65.5	13.0	491	1	Y084_MYCTU
35	65	12.9	344	1	TRD2_RALSO
36	65	12.9	399	1	YM96_SYNEL
37	65	12.9	462	1	A2AC_HUMAN
38	65	12.9	593	1	REGC_ECOLI
39	65	12.9	4377	1	ANK3_HUMAN
40	64.5	12.8	184	1	CYCM_BRAJA
41	64.5	12.8	320	1	Y678_METJA
42	64.5	12.8	750	1	ELS_CHICK
43	64.5	12.8	905	1	NUOG_PSEAE
44	64.5	12.8	1023	1	RT11_ACTPL
45	64.5	12.8	1023	1	RT12_ACTPL
46	64.5	12.8	1159	1	RPOC_PORCN
47	64.5	12.8	1608	1	HLVA_SERMA
48	64.5	12.8	2541	1	TLN1_HUMAN
49	64	12.7	246	1	HIS4_METMA
50	64	12.7	327	1	THI4_ASPOR
51	64	12.7	426	1	Y200_ANASP
52	64	12.7	487	1	DNA1_AGR5
53	64	12.7	555	1	YAGF_ECOLI
54	64	12.7	593	1	REGC_ECO57
55	63.5	12.6	82	1	C551_PSEME
56	63.5	12.6	130	1	F14A_HUMAN
57	63.5	12.6	130	1	RL7_MYCLE
58	63.5	12.6	230	1	FLGH_XANCP
59	63.5	12.6	345	1	TRPD_ABRPE
60	63.5	12.6	384	1	YGAY_ECO57
61	63.5	12.6	397	1	YGAY_ECOLI
62	63.5	12.6	407	1	AROC_MYCLE
63	63.5	12.6	432	1	YF10_MYCTU
64	63.5	12.6	541	1	Y4MM_RHISN
65	63.5	12.6	548	1	MERA_PSEFL
66	63.5	12.6	1048	1	P100_HCMVA
67	63.5	12.6	434	1	YU18_MYCTU
68	63	12.5	435	1	YU21_MYCTU
69	63	12.5	517	1	6PGD_CANAL
70	63	12.5	932	1	PMS1_HUMAN
71	63	12.5	1062	1	NAL2_HUMAN
72	63	12.5	267	1	THIG_DEIRA
73	62.5	12.5	361	1	COBT_MYCTU
74	62.5	12.5	511	1	NADP_CAUCR
75	62.5	12.5	560	1	EFS_MOUSE
76	62.5	12.5	760	1	CO2_MOUSE
77	62.5	12.5	128	1	RL7_CORGL
78	62	12.4	199	1	IL11_RAT
79	62	12.4	242	1	HIS4_HALN1
80	62	12.4	257	1	MOAE_KLEAE
81	62	12.4	257	1	G3P_DICLI
82	62	12.4	382	1	YN28_MYCTU
83	62	12.4	388	1	CHSD_PHANI
84	62	12.4	446	1	PCAB_PSEPU
85	62	12.4	620	1	SMP_COTUA
86	62	12.4	660	1	REP2_HUMAN
87	62	12.4	660	1	REP2_XANFL
88	62	12.4	660	1	YTX1_XENLA
89	62	12.4	675	1	YTX1_XENLA
90	62	12.4	829	1	E74B_DROME
91	62	12.4	883	1	E74B_DROME
92	62	12.4	954	1	GCSP_AGR5
93	62	12.4	954	1	RL7_BRUME
94	61.5	12.3	124	1	RLN2_AGR5
95	61.5	12.3	217	1	DDL_HAEIN
96	61.5	12.3	306	1	KLPP_XANCP
97	61.5	12.3	318	1	KLPP_XANCP
98	61.5	12.3	344	1	NAGK_HUMAN
99	61.5	12.3	355	1	TRPD_AZOBH
100	61.5	12.3	367	1	NK61_HUMAN

ALIGNMENTS

OS209	mycobacteri
Q8x800	raisthonia s
Q8dgm0	synchococc
P18825	homo sapien
P24230	escherichia
Q12955	homo sapien
P30323	bradyrhizob
Q58091	methanococ
P07916	gallus gall
Q910J6	pseudomonas
P55128	actinobacil
P55129	actinobacil
O33431	porphyromon
P15320	serratia ma
Q9Y490	homo sapien
Q8PWS2	methanosarc
Q9UWZ9	aspergillus
Q8Z098	anabaena sp
Q8U1H1	agrobacteri
P77596	escherichia
P76628	escherichia
P59918	prochloroco
Q9CCE6	mycobacteri
P71789	mycobacteri
P55572	rhizobium s
Q51772	pseudomonas
P08318	human cytom
P31500	mycobacteri
O53468	mycobacteri
O13287	candida alb
P54277	homo sapien
Q9NX02	homo sapien
Q9RYV1	deinococcus
Q10396	mycobacteri
Q9A4C3	caulobacteri
Q64355	mus muscucu
P21180	mus muscucu
Q8N228	corynebacte
Q99M55	rattus norv
Q9Hn14	halobacteri
P54795	klebsiella
Q94469	dictyosteli
P71884	mycobacteri
O22045	pharbitis n
P32427	pseudomonas
O33804	streptomyce
Q92154	coturnix co
O8NfH8	homo sapien
P51010	xanthobacte
P14380	xenopus lae
P20105	drosophila
P11536	drosophila
Q8Ufde	agrobacteri
P41106	brucella me
Q8Uhg2	agrobacteri
P44405	haemophilus
P23354	xanthomonas
Q8UJ70	homo sapien
P26944	azospirillu
P78426	homo sapien

```
UGR2 HUMAN
ID UGR2 HUMAN STANDARD; PRT; 104 AA.
AC Q96P01;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in
DE normal-1) (Secretoglobin family 3A member 1).
GN SCGB3A1 OR UGRP2 OR HIN1.
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396515; PubMed=11481438;
RA Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P.,
RA Kaelin C.M., Rhei E., Rosenberg M., Schnitt S., Marks J.R., Pagon Z.,
RA Belina D., Razumovic J., Polyak K.;
RT "HIN-1, a putative cytokine highly expressed in normal but not
RT cancerous mammary epithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21531978; PubMed=11682631;
RA Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
RA Kimura S.;
RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is
RT a novel lung-enriched downstream target gene for the T/EBP/NKX2.1
RT homeodomain transcription factor.";
RL Mol. Endocrinol. 15:2021-2036(2001).
CC -!- FUNCTION: Potential growth inhibitory cytokine.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- TISSUE SPECIFICITY: Highly expressed in breast tissues. Absent in
CC breast cancer cell lines.
CC -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF040564; AAK82942.1; -.
CC DR EMBL; AF313458; AAL26217.1; -.
CC DR Genew; HGNC:18384; SCGB3A1.
CC DR MIN; 606500; -.
CC DR GO; GO:0005576; C:extracellular; NAS.
CC DR GO; GO:0005125; F:cytokine activity; NAS.
CC DR GO; GO:0030308; P:negative regulation of cell growth; NAS.
CC DR GO; GO:0042127; P:regulation of cell proliferation; NAS.
CC KW Cytokine; Signal.
CC FT SIGNAL 1 20 POTENTIAL.
CC FT CHAIN 21 104 UTEROGLOBIN-RELATED PROTEIN 2.
CC FT CONFLICT 19 19 R -> A (IN REF. 2).
CC SQ SEQUENCE 104 AA; 10185 MW; 1083873C8FAE8015 CRC64;
Query Match 99.0%; Score 497; DB 1; Length 104;
Best Local Similarity 99.0%; Pred. No. 7.2e-36;
Matches 103; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 1 MKLAALGLCVALSASSAAFLVGSAPQVAPVAALESAAEAGAGTLANPLGTLNPKLL 60
DB 1 MKLAALGLCVALSASSAAFLVGSAPQVAPVAALESAAEAGAGTLANPLGTLNPKLL 60
QY 61 LSSLGIPVNHLEGSOKVAGLGPQAVGAVKALKALLGALTVEG 104
DB 61 LSSLGIPVNHLEGSOKVAGLGPQAVGAVKALKALLGALTVEG 104
```

RESULT 2

```
UGR2 MOUSE
ID UGR2 MOUSE STANDARD; PRT; 104 AA.
AC Q920D7;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Uteroglobin-related protein 2 precursor (Cytokine HIN-1) (High in
DE normal-1) (Secretoglobin family 3A member 1).
GN SCGB3A1 OR UGRP2 OR HIN1.
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21396515; PubMed=11481438;
RA Krop I.E., Sgroi D., Porter D.A., Lunetta K.L., LeVangie R., Seth P.,
RA Kaelin C.M., Rhei E., Rosenberg M., Schnitt S., Marks J.R., Pagon Z.,
RA Belina D., Razumovic J., Polyak K.;
RT "HIN-1, a putative cytokine highly expressed in normal but not
RT cancerous mammary epithelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 98:9796-9801(2001).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=21531978; PubMed=11682631;
RA Niimi T., Keck-Waggoner C.L., Popescu N.C., Zhou Y., Levitt R.C.,
RA Kimura S.;
RT "UGRP1, a uteroglobin/clara cell secretory protein-related protein, is
RT a novel lung-enriched downstream target gene for the T/EBP/NKX2.1
RT homeodomain transcription factor.";
RL Mol. Endocrinol. 15:2021-2036(2001).
CC -!- FUNCTION: Potential growth inhibitory cytokine.
CC -!- SUBCELLULAR LOCATION: Secreted (By similarity).
CC -!- SIMILARITY: Belongs to the uteroglobin family. UGRP subfamily.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; AF313456; AAL26216.1; -.
CC DR EMBL; MG1:191592; SCGB3A1.
CC KW Cytokine; Signal.
CC FT SIGNAL 1 21 POTENTIAL.
CC FT CHAIN 22 104 UTEROGLOBIN-RELATED PROTEIN 2.
CC SQ SEQUENCE 104 AA; 10591 MW; D62F0E601FB57A6D CRC64;
Query Match 49.8%; Score 250; DB 1; Length 104;
Best Local Similarity 57.0%; Pred. No. 8.2e-16;
Matches 61; Conservative 14; Mismatches 26; Indels 6; Gaps 4;
QY 1 MKLALGLCVALSASSAAFLVGS-APVAPVAALESAAEAGAGTLAN-PLGTLNPL 57
DB 1 MKLTTTFLVLCVALLSDSGVAFVMDSLAKPAVEPVAALEPAEAAVAGAVPSLPLSHLAIL 60
QY 58 KLLSSLGIPVNHLEGSOKVAGLGPQAVGAVKALKALLGALTVEG 104
DB 61 RFLTASMGIPDLPLEGSKKCVTELGPVAVGAV---KSLGLGLTMFG 104
RESULT 3
UGR1 HUMAN
ID UGR1 HUMAN STANDARD; PRT; 93 AA.
AC Q96P01;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 10-OCT-2003 (Rel. 42, Last annotation update)
DE Uteroglobin-related protein 1 precursor (Secretoglobin family 3A
DE member 2).
GN SCGB3A2 OR UGRP1.
```

Sequence Comparison

PR 18-AUG-1998; 98US-0096960P.  
 PR 18-AUG-1998; 98US-0097022P.  
 PR 19-AUG-1998; 98US-0097141P.  
 PR 20-AUG-1998; 98US-0097218P.  
 PR 24-AUG-1998; 98US-0097661P.  
 PR 26-AUG-1998; 98US-0097951P.  
 PR 26-AUG-1998; 98US-0097952P.  
 PR 26-AUG-1998; 98US-0097954P.  
 PR 26-AUG-1998; 98US-0097955P.  
 PR 26-AUG-1998; 98US-0097971P.  
 PR 26-AUG-1998; 98US-0097978P.  
 PR 26-AUG-1998; 98US-0097979P.  
 PR 26-AUG-1998; 98US-0097986P.  
 PR 26-AUG-1998; 98US-0098014P.  
 PR 31-AUG-1998; 98US-0098525P.  
 PR 16-SEP-1998; 98US-0100634P.  
 PR 12-JAN-1999; 99US-0115565P.

PA (GETH ) GENENTECH INC.

PI Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;  
 PI Wood WI, Yuan J;

XX WPI: 2000-072883/06.

DR N-PSDB; AA265103.

XX Membrane-bound proteins and related nucleotide sequences.

PT Claim 12; Fig 290; 822pp; English.

XX  
 CC The invention provides membrane-bound PRO polypeptides and  
 CC polynucleotides encoding them. The PRO sequences of the invention were  
 CC identified based on extracellular domain homology screening. The PRO  
 CC sequences have homology with proteins including LDL receptors, TIE  
 CC ligands and various enzymes. The membrane-bound proteins and receptor  
 CC molecules are useful as pharmaceutical and diagnostic agents. Receptor  
 CC immunoadhesins, for instance, can be used as therapeutic agents to block  
 CC receptor-ligand interactions. The membrane-bound proteins can also be  
 CC employed for screening of potential peptide or small molecule inhibitors  
 CC of the relevant receptor/ligand interaction. The PRO encoding sequences  
 CC are useful as hybridization probes, in chromosome and gene mapping and in  
 CC the generation of antisense RNA and DNA. PRO nucleic acid sequences will  
 CC also be useful for the preparation of PRO polypeptides, especially by  
 CC recombinant techniques

XX Sequence 104 AA;

Query Match 100.0%; Score 502; DB 3; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVALLSCSSAAAFVLSGAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLL 60  
 Db 1 MKLAALLGLCVALLSCSSAAAFVLSGAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLL 60  
 QY 61 LSSLGIPVNHLEIGSKCVAEFGPQAVGAVKALKALLGALTTFVG 104  
 Db 61 LSSLGIPVNHLEIGSKCVAEFGPQAVGAVKALKALLGALTTFVG 104

RESULT 2

AY44458  
 ID AAY44458 standard; protein; 104 AA.

AC AAY44458;

XX 27-MAR-2000 (first entry)

XX Human lung specific gene protein Lng107.

XX Lung Specific Gene; LSG; Lng107; human; diagnostic marker; prognosticate;  
 KW lung cancer; diagnosis.

## Sequence Comparison 'B'

XX Homo sapiens.  
 OS WO9960160-A1.  
 XX  
 PN 25-NOV-1999.  
 PD  
 XX 12-MAY-1999; 99WO-US010344.  
 PF  
 XX 21-MAY-1998; 98US-0086212P.  
 PR  
 XX (DIAD-) DIADEXUS LLC.  
 PA  
 PI Yang F, Macina RA, Sun Y;  
 XX WPI: 2000-116320/10.  
 DR N-PSDB; AA229723.  
 DR  
 XX A new method for diagnosing, monitoring and staging lung cancer.

PT Example 2; Page 38-39; 40pp; English.

PS The present sequence is a lung specific gene (LSG) protein Lng107 from

CC human clone ID 586271. The LSG has high level of tissue specificity for  
 CC lungs and is overexpressed in cancerous tissues. The sequence serves as a  
 CC diagnostic marker for detecting, monitoring, staging and prognosticating  
 CC lung cancer. The diagnosis involves comparing levels of LSG in samples  
 CC obtained from patient and normal control

XX Sequence 104 AA;

Query Match 100.0%; Score 502; DB 3; Length 104;  
 Best Local Similarity 100.0%; Pred. No. 1.4e-48;  
 Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLAALLGLCVALLSCSSAAAFVLSGAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLL 60  
 Db 1 MKLAALLGLCVALLSCSSAAAFVLSGAKPVAQPVAALESAAEAGAGTLANPLGTINPLKLL 60  
 QY 61 LSSLGIPVNHLEIGSKCVAEFGPQAVGAVKALKALLGALTTFVG 104  
 Db 61 LSSLGIPVNHLEIGSKCVAEFGPQAVGAVKALKALLGALTTFVG 104

RESULT 3

AY87288  
 ID AAY87288 standard; protein; 104 AA.

AC AAY87288;

XX 11-MAY-2000 (first entry)

XX Human signal peptide containing protein HSP65 SEQ ID NO:65.

DE Human; signal peptide-containing protein; HSP65; diagnosis; cancer;  
 KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;  
 KW antimicrobial; neutropenic; neuroprotective; cardiovascular; hepatotropic;  
 KW antitastmatic; gene therapy; cell proliferation; neurological disorder;  
 KW reproductive disorder; developmental disorder; arteriosclerosis;  
 KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;  
 KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;  
 KW Parkinson's disease; Huntington's disease; ovulatory defect;  
 KW muscular dystrophy.

OS Homo sapiens.

XX WO200000610-A2.

PN 06-JAN-2000.

XX 25-JUN-1999; 99WO-US014484.

XX 26-JUN-1998; 98US-0090762P.

## Sequence Comparison 'C'

see over

**Sequence Comparison**

Query Match  
Best Local Similarity 100.0%; Score 502; DB 3; Length 104;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLALLGLCVALSCTSSAAAFVLSGAKVPVAALFSAAGAGTIANPLGTINPKLL 60  
DB 1 MKLALLGLCVALSCTSSAAAFVLSGAKVPVAALFSAAGAGTIANPLGTINPKLL 60  
QY 61 LSSLGIPVNHLIEGSKVKVAELGPQAVGVKALKALLGALTIVFG 104  
DB 61 LSSLGIPVNHLIEGSKVKVAELGPQAVGVKALKALLGALTIVFG 104

RESULT 4  
AAB65280  
ID AAB65280 standard; protein; 104 AA.  
XX AC AAB65280;  
XX DT 02-APR-2001 (first entry)  
XX DE Human PRO1245 (UNG629) protein sequence SEQ ID NO:408.  
XX DX Human; secreted and transmembrane protein; PRO; cytotostatic; cell death;  
KW cancer; chromosomal mapping; gene mapping; tissue typing;  
XX diagnostic assay.

31-JUL-1998; 98US-0094983P.  
01-OCT-1998; 98US-0102686P.  
11-DEC-1998; 98US-0112129P.  
(INCYTE-) INCYTE PHARM INC.  
Lal P, Tang YT, Gorgone GA, Corley NC, Guegler KJ, Baughn MR;  
Akerblom IE, Au-Yang J, Yue H, Patterson C, Reddy R, Hallman JL;  
Bandman O;  
WPI; 2000-160673/14.  
N-PSDB; AAZ98173.  
New human signal peptide-containing proteins useful in treatment,  
prevention and diagnosis of e.g. cancer, inflammation and cardiovascular  
disease.  
Claim 1; Page 206; 327pp; English.  
AAZ98109 to AAZ98242 encode AY87224 to AY87357 which represent the  
human signal peptide-containing proteins HSPP-1 to HSPP-134. HSPPs have  
anticancer, anti-inflammatory, antimicrobial, neoplastic, hepatotropic,  
neuroprotective, cardiovascular and antiaesthetic activities, and can be  
used in gene therapy. HSPPe can be used to treat or prevent disorders  
associated with decreased activity or function of HSPP. Antagonists of  
HSPP are used to treat or prevent disorders associated with increased  
activity or function of HSPP. Such diseases include cell proliferation  
(including cancer), inflammation, cardiovascular, neurological,  
reproductive or developmental disorders, (e.g. arteriosclerosis,  
cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,  
asthma, Crohn's disease, Alzheimer's, Parkinson's or Huntington's  
ischaemic heart disease, microbial or other infections, congestive or  
diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSPP  
nucleic acids can be used for the recombinant production of HSPP, for  
detecting HSPP in standard hybridisation and amplification assays (for  
diagnosis and monitoring), in gene therapy, as antisense, triplex-forming  
or ribozyme therapeutics, for detecting related sequences or genetic  
variations, and for chromosomal mapping. HSPP are also used to raise  
specific antibodies (Ab) and to screen for agonists and antagonists  
(potential therapeutic agents). Ab are used to diagnose, or monitor, HSPP  
-related diseases (in usual immunoassays), as therapeutic antagonists, in  
competitive drug screens, and for purification of HSPP from natural  
sources

Sequence 104 AA;  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 3; Length 104;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLALLGLCVALSCTSSAAAFVLSGAKVPVAALFSAAGAGTIANPLGTINPKLL 60  
DB 1 MKLALLGLCVALSCTSSAAAFVLSGAKVPVAALFSAAGAGTIANPLGTINPKLL 60  
QY 61 LSSLGIPVNHLIEGSKVKVAELGPQAVGVKALKALLGALTIVFG 104  
DB 61 LSSLGIPVNHLIEGSKVKVAELGPQAVGVKALKALLGALTIVFG 104

RESULT 4  
AAB65280  
ID AAB65280 standard; protein; 104 AA.  
XX AC AAB65280;  
XX DT 02-APR-2001 (first entry)  
XX DE Human PRO1245 (UNG629) protein sequence SEQ ID NO:408.  
XX DX Human; secreted and transmembrane protein; PRO; cytotostatic; cell death;  
KW cancer; chromosomal mapping; gene mapping; tissue typing;  
XX diagnostic assay.

OS Homo sapiens.  
XX WO2000073454-A1.  
XX PD 07-DEC-2000.  
XX PF 30-MAR-2000; 2000WO-US008439.  
XX PR 02-JUN-1999; 99WO-US012252.  
PR 23-JUN-1999; 99US-0141037P.  
PR 07-JUL-1999; 99US-0143048P.  
PR 26-JUL-1999; 99US-0144758P.  
PR 28-JUL-1999; 99US-0145698P.  
PR 17-AUG-1999; 99US-0146222P.  
PR 15-SEP-1999; 99WO-US021090.  
PR 08-OCT-1999; 99WO-US021547.  
PR 30-NOV-1999; 99WO-US028313.  
PR 01-DEC-1999; 99WO-US028301.  
PR 16-DEC-1999; 99WO-US03009S.  
PR 20-DEC-1999; 99WO-US030911.  
PR 05-JAN-2000; 2000WO-US000219.  
PR 06-JAN-2000; 2000WO-US000376.  
PR 11-FEB-2000; 2000WO-US003565.  
PR 18-FEB-2000; 2000WO-US004341.  
PR 22-FEB-2000; 2000WO-US004414.  
PR 24-FEB-2000; 2000WO-US004914.  
PR 02-MAR-2000; 2000WO-US005004.  
PR 15-MAR-2000; 2000WO-US005841.  
PR 20-MAR-2000; 2000WO-US007377.  
(GETH ) GENENTECH INC.  
ASKENAZI AJ, Baker KP, Bofstein D, Desnoyers L, Eaton DL;  
Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski RJ;  
Grimaldi CJ, Gurney AL, Kijavini IO, Napier MA, Pan J, Paoni NF;  
Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;  
Zhang Z;  
WPI; 2001-032160/04.  
N-PSDB; AAF44249.  
PRO polynucleotides used to produce polypeptides used to target bioactive  
molecules such as toxins, radiolabels or antibodies, to specific cells,  
to cause targeted cell death.  
Claim 12; Fig 280; 935pp; English.  
The present invention describes human secreted and transmembrane PRO  
proteins. The PRO proteins have cytostatic activity. The PRO proteins can  
be used for targeted delivery of bioactive molecules, such as toxins,  
radiolabels or antibodies, that cause cell death. PRO nucleotide  
sequences, and their fragments, can be used as hybridisation probes, in  
chromosomal and gene mapping, and in the generation of anti-sense RNA and  
DNA. They may also be used to produce transgenic animals which are used  
to develop and screen therapeutically useful reagents. The PRO nucleotide  
and protein sequence can be used for tissue typing and in treating  
cancer. Anti-PRO antibodies can be used in diagnostic assays. AAF44270 to  
AAF44470 represent PCR primers and hybridisation probes used in the  
isolation of human PRO sequences. AAF44087 to AAF44369 and AAB65154 to  
AAB65300 represent human PRO polynucleotide and protein sequences given  
in the exemplification of the present invention  
Sequence 104 AA;  
Query Match  
Best Local Similarity 100.0%; Score 502; DB 4; Length 104;  
Matches 104; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MKLALLGLCVALSCTSSAAAFVLSGAKVPVAALFSAAGAGTIANPLGTINPKLL 60

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OM protein - protein search, using sw model

Run on: April 5, 2004, 14:09:33 ; Search time 54 Seconds  
(without alignments)

544.166 Million cell updates/sec

Title: US-09-997-428-408

Perfect score: 502

Sequence: 1 MKLAALGLCVALLSCSAAA.....QAVGAVKALKALIGALTIVFG 104

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : A\_Geneseq\_29Jan04.\*

1: Geneseqp1980s.\*

2: Geneseqp1990s.\*

3: Geneseqp2000s.\*

4: Geneseqp2001s.\*

5: Geneseqp2002s.\*

6: Geneseqp2003as.\*

7: Geneseqp2003bs.\*

8: Geneseqp2004s.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	502	100.0	104	3	AAV66757 Membrane-
2	502	100.0	104	3	AAV44458 Human lun
3	502	100.0	104	3	AAV87288 Human sig
4	502	100.0	104	4	AB65280 Human PRO
5	502	100.0	104	5	AAU86141 Human PRO
6	502	100.0	104	5	AAU86141 Human PRO
7	502	100.0	104	6	ABU58095 Human PRO
8	502	100.0	104	6	ABU59173 Novel hum
9	502	100.0	104	6	ABU82685 Human sec
10	502	100.0	104	6	AAO19895 Human ute
11	502	100.0	104	6	ABU60604 Human sec
12	502	100.0	104	6	ABU13986 Human PRO
13	502	100.0	104	6	ABU72571 Novel hum
14	502	100.0	104	6	ABU59320 Human sec
15	502	100.0	104	6	ABU26017 Human PRO
16	502	100.0	104	6	ABU59026 Human sec
17	502	100.0	104	6	ABU92404 Novel hum
18	502	100.0	104	6	ABU59469 Novel hum
19	502	100.0	104	6	ABU10941 Human PRO
20	502	100.0	104	6	ABU81693 Novel hum
21	502	100.0	104	6	ABU88632 Human sec
22	502	100.0	104	6	ABO34146 Human PRO
23	502	100.0	104	6	ADA37919 Human sec
24	502	100.0	104	6	ADA21605 Human sec
25	502	100.0	104	6	ADA10392 Human sec

26	502	100.0	104	6	ADA17936	Human PRO
27	502	100.0	104	6	ADA28044	Human sec
28	502	100.0	104	6	ADA94624	Human sec
29	502	100.0	104	6	ADA38849	Human sec
30	502	100.0	104	6	ADA92970	Human sec
31	502	100.0	104	7	ABO53232	Human sec
32	502	100.0	104	7	ADA22531	Human sec
33	502	100.0	104	7	ABO22602	Human sec
34	502	100.0	104	7	ADA06697	Human sec
35	502	100.0	104	7	ADA39390	Human PRO
36	502	100.0	104	7	ADB96416	Human PRO
37	502	100.0	104	7	ADC57888	Human PRO
38	502	100.0	104	7	ADC55252	Human PRO
39	502	100.0	104	7	ADC12119	Human sec
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41	502	100.0	104	7	ADC07596	Human sec
42	502	100.0	104	7	ADC11586	Human sec
43	502	100.0	104	7	ADC14708	Novel hum
44	502	100.0	104	7	ADD08240	Novel hum
45	502	100.0	104	7	ADD82085	Human PRO
46	502	100.0	104	7	ADD07707	Novel hum
47	502	100.0	104	7	ADD82598	Human PRO
48	502	100.0	104	7	ADD08778	Novel hum
49	502	100.0	104	7	ADD07027	Novel hum
50	502	100.0	104	7	ADC83274	Human PRO
51	502	100.0	104	7	ADP55381	Human PRO
52	502	100.0	104	7	ADD56339	Human PRO
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54	502	100.0	104	7	ADE26931	Novel hum
55	502	100.0	104	7	ADE26398	Novel hum
56	498	99.2	104	2	AAW75868	Novel hum
57	250	49.8	104	2	AAO19893	Murine ut
58	160	31.9	93	2	AAW62068	Human lun
59	160	31.9	93	2	AAV28334	LJL03 spe
60	160	31.9	93	3	AAV44456	Human lun
61	160	31.9	93	3	AAV87289	Human sig
62	160	31.9	93	4	AAU29145	Human PRO
63	160	31.9	93	6	ABU58521	Human PRO
64	160	31.9	93	6	ABU88069	Novel hum
65	160	31.9	93	6	ABU84384	Human sec
66	160	31.9	93	6	ABR6258	Human sec
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68	160	31.9	93	6	ABU9588	Human sec
69	160	31.9	93	6	ABU82827	Human PRO
70	160	31.9	93	6	ABU89948	Novel hum
71	160	31.9	93	6	ABR68197	Human sec
72	160	31.9	93	6	AAO19894	Human ute
73	160	31.9	93	6	ABU96250	Novel hum
74	160	31.9	93	6	ABU2681	Human sec
75	160	31.9	93	6	ABO08758	Human sec
76	160	31.9	93	6	ABO02810	Human sec
77	160	31.9	93	6	ABR74964	Human sec
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82	160	31.9	93	6	ABU91780	Novel hum
83	160	31.9	93	6	ABU89473	Human PRO
84	160	31.9	93	6	ABU86314	Human sec
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88	160	31.9	93	6	ABR98863	Human sec
89	160	31.9	93	6	ABO16386	Human sec
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92	160	31.9	93	6	ABR78348	Human sec
93	160	31.9	93	6	ABU85084	Novel hum
94	160	31.9	93	6	ABO00223	Novel hum
95	160	31.9	93	6	ABO11555	Human sec
96	160	31.9	93	6	ABO02200	Human sec
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98	160	31.9	93	6	ABU83469	Human sec

Abo06270 Novel hum  
Abr59306 Human sec99 160 31.9 93 6 ABO06270  
100 160 31.9 93 6 ABR59306

## ALIGNMENTS

## SEQUENCE COMPARISON

RESULT 1  
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ID AAY66757 standard; protein; 104 AA.

XX AAY66757;

XX 05-APR-2000 (first entry)

XX Membrane-bound protein PRO1245.

XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;  
KW pharmaceutical; receptor immunoadhesin; gene mapping.

XX Homo sapiens.

XX WO9963088-A2.

XX 09-DEC-1999.

XX 02-JUN-1999; 99WO-US012252.

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XX 03-JUN-1998; 98US-0087827P.

XX 04-JUN-1998; 98US-0088021P.

XX 04-JUN-1998; 98US-0088025P.

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